GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 25, 2000, 14:25:02; Search time 28.15 Seconds (without alignments) 337.411 Million cell updates/sec

US-09-391-958-1 401

Title: Perfect score: Sequence:

1 MQVDETLIPRKVPSLCSARY......LIFGEADVQEWAKERKLTRL 401

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 188963 seqs, 23686106 residues

Word size : 0

Total number of hits satisfying chosen parameters:

188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	w	2	–	Result No.
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	و	241		Score
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Eat-4 protein amin	Human sodium-lithi	Human brain sodium	CLYTA-E6E7-His pro	Prot.D1/3-E6-E7-Hi	Human macrophage/d	መ	Human chemokine re	Pig kidney cell mu	Porcine mutarotase	Human papilloma vi	HPV 16 E7 protein	Amino terminal CTL	Amino terminal CTL	CTLA4-E7 fusion pr	fus	- 1	ProtDthr126-E7-His	Prot.D1/3-E7-mut(C	Papillomavirus E7/	Human papilloma vi			E7	lney cell	Mouse T118 Flt3 li	api	HPV-16 E7 peptide.	Immunopeptide #2 d	Vitamin E transpor	Human haemochromat	Human haemochromat	Š	Description .

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67 1 W73466	64 1 Y07882	43 6 1.5 47 1 P94146 Am	40 1 R96006	6 1.5 33 1 W40008	6 1.5 24 1 R33151	6 1.5 22 1 W06566	1 W36605	6 1.5	6 1.5 13 1 R10628	1 R33150	7 1.7 671 1 R85290 S	
Human secreted pro	Human secreted pro	Amino acid sequenc	Asymmetry sequence	Peptide effecting	HPV E7 protein - R	Human preprocollag	Human E-Cadherin v	Human wild-type E-	Human Papilloma Vi	HPV E7 protein - R	Streptococcus faec	

ALIGNMENTS

Qy	Дb	γΩ	Db	γQ		
	ون -	9			Matches	Query Match
121 ILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYIISSLKQQ 180	61 SEVLPVDSFGGLSKAPKSLPAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGCFTA 120	61 SEVLPVDSFGGLSKAPKSLPAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGCFTA 120	1 MQVDETLIPRKVPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDS 60	1 MQVDETLIPRKVPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDS 60	Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps	Match 100.0%; Score 401; DB 1; Length 401;
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                                                                                                                                                                                    The present invention describes hereditary haemochromatosis gene CC products from the human haemochromatosis gene. Also described is a CC method to determine the presence or absence of the common hereditary cCC haemochromatosis (HFE) gene mutation in an individual comprising: CC presence or absence of the presence or absence of a haplotype or genotype where CC the presence or absence of the haplotype genotype indicates the likely creamed an acceptable of the HFE gene mutation in the genome of the individual. The CC presence of the HFE gene mutation in the genome of the individual. The CC presence sequences from the present invention can be used to develop counts for use in the diagnosis and treatment of HFE. The present cc invention also describes BTF genes, which are homologues of the milk CC protein butyrophilin (BT), and can be used in the production of agonists considered are: (1) a RoRet gene CC which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NFT3 and NFT4 genes which are homologues of a type 1 sodium transport gene, and can cc similarly be used for hypophosphatemia. The present sequence represents
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                                                                                                            Query Match
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07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                161 SYPWISTSEKEYIISSLKQQVGSSKQPLPIKAMLRSLPIWSICLGGFSHQWLVSTMVVYI 220
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Tsuchihashi Z, Wolff RK;
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Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3;
BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
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21-DEC-1998 (first entry)
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                                                                                            Local Similarity
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ŞYPWISTSEKEYIISSLKQQVGSSKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYI 220
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                                                                             Conservative
                                                                                          60.1%;
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Pred. No. 9.7e-237;
                                                                       Mismatches
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OF GENERAL RESTRICTION OF STATES AND SOURCE 
                                   The present invention describes hereditary haemochromatosis gene comethod to determine the presence or absence of the common hereditary comethod to determine the presence or absence of the common hereditary comethod to determine the presence or absence of the presence or genotype the common hereditary comethod to determine the presence or absence of the presence of the presence of the presence of the haplotype genotype indicates the likely comesence of the haplotype genotype where comesence of the haplotype genotype indicates the likely comesence of the HFE gene mutation in the genome of the individual. The company of the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists come and antagonists of BT function. Also described are: (1) a Roret gene company of the sued to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NFP3 and NFP4 genes similarly be used for hypophosphatemia. The present sequence represents
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30-SEP-1997; U17658.
30-SEP-1997; US-852495.
07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
(PROG-) PROGENTIOR INC.
Feder JN, Kronmal GS, Lau
Tsuchhhashi Z, Wolff RK;
Sequence
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Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 54; Fig 5B; 209pp; English
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Query Match Best Local Matches

Similarity 9; Conserv

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PR 11-MAY-1996; SE-001705.

PR 11-MAY-1996; SE-001705.

PR 11-MAY-1996; SE-001705.

PR MEDS-) MEDSCAND AB.

PR MEDS-) MEDSCAND AB.

PR Dillner J, Dillner L, Cheng HM;

PI Disquosis of human papilloma virus infection and PV-carrying pr antigen-antibody complexes by immunoassay

PT antigen-antigen-antigen-antigen-antigen-antigen-antigen-antigen-antigen-antigen-antigen-antigen
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23-MAY-1991; 146564.
23-MAY-1991; JP-146564.
(EISA) EISAI CO LTD.
WPI; 94-071958/09.
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Vitamin=E-specific transport protein(s) - are effective transporters of vitamin=E claim I; Page 8; 8pp; Japanese.
This is the partial sequence of a vitamin E transport protein. transport protein also comprises the partial sequence described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O2-MAR-1992 (first entry)
Immunopeptide #2 derived from HPV16 E7 peptide.
cervical cancer; cervical intraepithelial neoplasia;
squamous cell carcinoma; ELISA; HPV 16.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R56478 standard;
R56478;
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   R31212
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                                                                                                                                                                                                              QLNDSSE 62
                                                                                                                                                       QLNDSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
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7; Conser
   standard; peptide;
                                                                                                                                                                                                                                                                           Similarity 100
7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein fragment.
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                                                                                                                                                                                                                                                                    1.7%;
100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                           Score 7; L
Pred. No.
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Matches
            Query Match
Best Local
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27-AUG-1997: 037409.
27-AUG-1997: DE-037409.
(MEDI-) MEDIGENE AG.
HOEPFI R:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of HPV-16 E6 and E7-gene derived peptide(s) and their specific antibodies - for treatment and diagnosis of HPV-16 associated invasive cervical cancer pisclosure; Page 7; 14pp; English. The peptide represents an epitope of the human papillomavirus type 1 protein, from amino acids 6-35. This epitope is useful as a target for diagnosis and imaging of HPV-associated cancers, such as invasive cervical cancer. Antibodies raised against this epitope, tagged with cytotoxic molecules, such as cholera toxin, have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigens; diagnostic; cytotox Human papillomavirus type 16. EP-523391-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-1992; 110367.
13-JUL-1991; EP-111720.
(BEHW ) BEHRINGWERKE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPV-16 E7 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R31212;
19-MAY-1993
                                                          Disclosure; Column 3; 4pp; German.

This invention describes peptides used in a diagnosis kit for testing skin for immune reactions against onco-protein E6 and E7. The method of the invention comprises onco-protein E6 and E7 and/or immunologically active parts of E6 and E7 derived from human papilloma virus.

Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tagged with cytotoxic molecules, therapeutic potential. See also R31213-5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                 Diagnosis kit for testing skin for immune reactions against onco-protein E6 and E7 comprises onco-protein E6 and E7 comprises onco-protein E6 and E7 computed from human immunologically active parts of E6 and E7 derived from human papilloma virus
Disclosure; Column 3; 4pp; German.
                                                                                                                                                                                                                                                                                     Human papillomavirus.
DE19737409-A1.
                                                                                                                                                                                                                                                                                                                Human papillomavirus pep
Diagnosis; skin; immune
                                                                                                                                                                                                                                                                                                                                                                    W93288
                                                                                                                                                                                                      WPI; 99-168276/15.
                                                                                                                                                                                                                                                                                                                                           27-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 QLNDSSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                    standard; peptide; 30
Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
1.7%; Score 7;
llarity 100.0%; Pred. No.
Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E7; epitope; cervical cancer; invasive; cytotoxic; tagged.
                                                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                 reaction; onco-protein; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                 fragment #2.
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    Mismatches
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     Indels
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R66178

AC R66278

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R72968
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New ligand for the Flt3 tyrosine kinase receptor - and related in nucleic acid, vectors, host cells and antibodies, useful for treating abnormal cell physiology and proliferation, e.g. cancer, it is a for diagnosis and drug screening claim 11; page 80; 90pp; English.

A CDNA library from the human stromal cell line 295V48, in pwil8s, was screened with an 800 bp fragment derived from conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 20 conserved between two mouse clones, T118 and T110. Approx. 75% homologous to the mouse clones over the first 163 AAs. Clone S86 continued to the mouse clones over the first 163 AAs. Clone S86 continued continued lesser degree, for an overall homology of 668. Clones T118 and Clones after mouse residue 163 (human residue 160). An additiona mouse clone designated M88 has a 29 AA insert at the junction between the common and divergent portions of the mouse ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      # Flt3 ligand; tyrosine kinase receptor ligand; ss Mus musculus.

# W09426891-A.

24-NOV-1994.

18-MAY-1994; U05150.

19-MAY-1993; US-065231.

R 19-MAY-1993; US-089263.

R 16-JUL-1993; US-089263.

R 16-JUL-1993; US-092649.

R 24-AUG-1993; US-113391.

R 13-NUC-1993; US-15111.

R 03-DEC-1993; US-152413.

A (INRM ) INST NAT SANTE & RECH MEDICALE.

SCHEE JS CHERING CORP.

T Dittaling CH TIGE FD.
                                                                                                                                                                                       13-SEP-1994.
26-FEB-1993; 062646.
26-FEB-1993; JP-062646.
(AMAN ) AMANO PHARM KK.
(AMAN ) 5-181575/24.
Example 1; Page 6; 7pp; Japanese.

Example 1; Page 6; 7pp; Japanese.

The amino acid sequences (R72965-8) are internal protease digested fragments of the mutarotase protein from pig kidney cells (R72964) (R72964).
                                                                                                                                           mutarotase
                                                                                                                                                               Mutarotase gene - useful for
                                                                                                                                                                                                                                                                                                                                        Sus scrofa.
J06253856-A.
                                                                                                                                                                                                                                                                                                                                                                               Pig kidney cell mutarotase peptide fragment LY-15 Mutarotase; pig; kidney; aldose-1 epimerase; catai glucose; lambda library; probe; pBluescript; E.co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R72968 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 TATALLT 304
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Flt3 ligand pep
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100.0%; Pr
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                                                                                                                                                       the efficient mass
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                                                                                                                                                                                                                                                                                                                                                                                     pBluescript; E.coli.
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                                                                                                                                                                                                                                                                                                                                                                                                       catalytic conversion;
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Best Local :
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02-APR-1992.
26-SEP-1991; U07081.
26-SEP-1990; US-588384.
(BRIM ) BRISTOL-MYERS SQ
Blake J, Chen L, Hellstr
         21-MAY-1994 (first entry)
Human papillomavirus 16 E7 protein and fragments.
Tumours; cows; horses; donkeys; regression; udder
                                                    R42361;
                                                                                                                                                                                                                                                resulting from HPV
See also R22766.
Sequence 98 AA;
                                                                                                                                                                                                                                                                              The peptide is the sequence of the human papillomavirus HPV 16 E7 nucleoprotein. Peptides corresponding to regions (pref. epitopic regions) of HPV 16 E7 were synthesised by standard Merrifield synthesis. Examples of such peptides are E7 1-10, 29-50 or 70-81. Compositions conto. these peptides, antibodies against the peptides, or recombinant cells conto. the gene encoding the immunogenic peptides may be utilised in methods for inhibiting and treating HPV prevention or retardation of cervical warts and cervical carcinoma
                                                             R42361 standard;
                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 7; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                    prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic peptide(s) and recombinant cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thomas E K;
WPI; 92-132119/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; papillomavirus; immunogenic; cervical; warts; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of alpha-D-glucose to beta-D-glucose. This fragment corresponds to amino acids 145-231 of the entire protein. The peptides were generated by digestion with trypsin, chemotrypsin, endopeptidase and Staphylococcus v8 protease. The gene was isolated from a pig kidney cell cDNA lambda library using the probe Q85958. The gene was inserted into the plasmid pBluescript II and transformed into E.coli JM109 for production of the
                                                                                                                                                                                                                                                                                                                                                                                                                         infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPV E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R22767 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                               27
                                                                                                                                                       56 QLNDSSE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VDETLIP 9
                                                                                                                               QLNDSSE
                                                                                                                                                                                 Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                            1.7%; So ilarity 100.0%; F Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 of cervical warts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 AA;
                                                                                                                               \mathfrak{S}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYERS SQUIB. Hellstrom I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               encoding
        donkeys;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived
                                                             98
                                                                                                                                                                            Score 7; DB 1; Pred. No. 15; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 7; DB 1
Pred. No. 14;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hellstrom K,
                                                                                                                                                                                                                                                                                                                                                                                                                                             from them,
        regression;
                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer
                                                                                                                                                                                                                                                                                                                                                                                                                             E6 or E7 region of HPV16, useful in treatment and ncer resulting from HPV
                                                                                                                                                                                         DB 1;
). 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
. 14;
     udder warts; HPV16
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                                                                                                                                                                                                     98
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                                                                                                                                                                        Gaps
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Synthetic.

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W46886
ID W44
AC W44
AC
δõ
                                                                                                                                                                                                                                                   PT Evaluation of proliferative state of cells transformed with human PT papilloma virus - by determining cyclin-dependent kinase activity PT induced by E7 onco-protein
PT papilloma virus - by determining cyclin-dependent kinase activity PT induced by E7 onco-protein
PS Disclosure; Columns 19-20; 14pp; English.

CC E7 oncoprotein. The proliferative state of a cell transformed with CC kinase complexes containing protein papillowing manner. Cyclin/cyclin-dependent CC kinase complexes containing protein palCIPI (W46887-88) are isolated CC from the transformed cell, and the HPV E7 oncoprotein added to the CC isolated protein. Cyclin/cyclin-dependent kinase complexes are isolated CC from an untransformed cell that is substantially homogenic with the CC transformed cell, and the HPV E7 oncoprotein added. The kinase activities of the 2 samples are measured, where a proliferating transformed cell has a greater kinase activity that the untransformed cell. The method is cused for determining the extent of interaction and/or inactivation CC between a cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and thus evaluating the proliferative state of a transformed cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Best Local S
Matches 7
                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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17-MAR-1995;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-1998 (first entry)
Amino acid sequence of the HPV-16 E7 oncoprotein.
E7 oncoprotein; proliferative state; HPV; kinase activity;
E7 cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;
cyclin/cyclin-dependent kinase inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type 4.
See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones DL, Munger K;
WPI; 98-239202/21.
N-PSDB; V16717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of horses or donkeys
Disclosure; Fig 2; 31pp; English.
The sequence is that of the human papillomavirus type 16 E7 protein.
The protein sequence was aligned with that of bovine papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of papilloma-virus E7 protein or fragments for the therapy of papilloma-virus disease - for the regression of tumours e.g. removal of warts from udders or mouth of milking cows or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09320844-A.
28-OCT-1993.
01-APR-1993; G00679.
08-APR-1992; GB-007701.
(CANC-) CANCER RES CAMPAIGN TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAR-1995; US-406248.
(HARD ) HARVARD COLLEGE.
(HARD ) UNIV HARVARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campo MS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W46886 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 93-351368/44.
   56 QLNDSSE 62
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les 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              papillomavirus
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98 AA;
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llarity 100.0%;
Conservative
                                                            Conservative
                                                1.7%; 500
100.0%; Pr
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RESULT
W99370
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R97562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  variants of E6 and/or E7 protein, pref. deletion mutants, and are used to treat or prevent HPV infection

Example 3; Page 17; 37pp; English.

A variant of the human papilloma virus (HPV) E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a deletion mutant comprising at least half, and preferably two-thirds of full length E6 or E7 protein starting from the N- or C-terminal, or is a full length E6 molety fused to a full length E7 molety. The variant optionally has a linkage moicty and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This is a fusion protein of the C-terminal end of E6 and the N-terminal end of E7. The protein is also a deletion mutant generated from the sequence described in T31833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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20-DEC-1995; AU0868.
20-DEC-1994; AU-000157.
(CSLC-) CSL LTD.
(UYQU ) UNIV QUEENSLAND.
(UYQU ) UNIV QUEENSLAND.
(COX J. Edwards SJ. Fraz
WPI: 96-309518/31.
                       Antitumour composition containing immunogenic polypeptide with altered localisation - or vector expressing this polypeptide, particularly for treating or preventing cervical cancer association with human papilloma virus
                                                                                                                                                                                                                                                                                                                               signal peptide; papillomavirus; infection;
Chimeric - Human papillomavirus.
Chimeric - Rabies virus.
                                                                                                                                     (TRGE ) TRANSGENE SA.
Balloul JM, Bizouarne
WPI; 99-132161/11
                                                                                                                                                                                                                                                                                                                                                                                                                      Papillomavirus E7/glycoprotein signal peptide fusion protein Antitumour; immunogen; intracellular localisation; cancer; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W99370
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Vaccine variants of human papilloma virus antigens - contain variants of E6 and/or E7 protein, pref. deletion mutants, and
                                                                                                                                                                                                                      28-JAN-1999.
17-JUL-1998; F01576.
18-JUL-1997; FR-009152.
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Human papilloma virus E6/E7 protein variant.
Human papilloma virus; E6; E7; deletion mutant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-MAY-1999 (first entry)
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125 QLNDSSE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; peptide; 185
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172
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                                                                                                                                                                  ž
74pp; French
                                                                                                                                                                  Kieny MP;
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Pred. No.
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27;
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RESULT 15
Y02634
ID Y02634
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DT 22-UNI
DE PROT.C
KW Chimer
OS Chimer
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IPN W0991(
PD 04-MAF
PF 17-AU(
PA (SMIK
PI Bruck
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PI Human
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                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                             Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for treatment or prophylaxis of HPV induced lesions
Disclosure; Fig 8; 95pp; English.
This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for malignant) and preventing HPV viral infection.
Sequence 220 AA;
56 QLNDSSE 62
|||||||
140 QLNDSSE 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lombardo-Bencheikh A; WPI; 99-190587/16. N-PSDB; X29783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-JUN-1999 (first entry)
Prot.Dl/3-E7-mut(C24G,E26Q)/HPV16 protein.
Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy; tumour; lesion; benign; mailgnant; virus; infection.
Chimeric - Human papillomavirus.
Chimeric - Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an antitumour composition containing a therapeutic or prophylactic agent or one or more immunogenic polypeptides, where at least one polypeptide is modified so that its intracellular localisation is different from that of the native polypeptide. This sequence represents an example of a modified immunogenic protein and corresponds to the E7 protein from human papillomavirus fused to the rables virus glycoprotein signal peptide. The compositions, vectors and particles are used to treat or prevent cancers and tumours, specifically those associated with papillomavirus infection (e.g. cancer or low grade dysplasia of the cervix uteri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-MAR-1999.
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22-AUG-1997;
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100.0%; Pr
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o. 34;
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Search completed: May 25, 2000, 14:54:02 Job time: 1740 sec

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Sequence

20, Appl 48, Appl 20, Appl 20, Appl 20, Appl 185, Appl 185, Appl 11, Appl 1

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Post-processing: Listing first 45 summaries
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
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US-08-724-394A-10
US-08-363-586-1
PCT-US94-05150-22
US-08-465-078-20
US-08-465-078-20
US-08-465-078-20
US-08-468-062-20
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US-08-647-481-2
US-08-4647-481-2
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US-08-647-481-2
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                                    sequence
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     Sequence
Sequence
 11, Appli 10, Appli 11, Appli 11, Appli 12, Appli 20, Ap
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; CLONE: 754412
US-08-805-118-1
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US-08-805-118-1
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     Matches 401;
                  Query Match
Best Local Similarity
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MEDIUM TYPE: Diskette

COMPUTER: IEM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 415-855-0555
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STREET: 31/2
CITY: Palo Alto
CTATE: CA
TTATE: TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/805,118
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lal, Preet1
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                           IMMEDIATE SOURCE:
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TOPOLOGY: 11
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US-08-36-110A-48
US-08-326-110A-48
US-08-634-641-20
US-09-249-471-20
US-08-05-3-131-1185
US-08-09-762-185
PCT-US93-07213-13
US-08-497-233-11
PCT-US93-06643-11
PCT-US93-06643-11
PCT-US93-06643-11
US-08-441-629-16
PCT-US95-09172-16
US-08-438-439C-21
US-08-236-427-4
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Result

Score

0

Gaps

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Minimum Maximum

DB DB

Word size :

Database :

Title: Perfect score:

Run on:

Scoring table: Sequence:

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RESULT 2
US-08-724-394A-11
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GENERAL IN
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                                                       TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 11:
                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 01
                                         SEQUENCE CHARACTERISTICS:
                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Megabase Transcript Map: No. 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
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ZIP: 94111-3834
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                                                                                                                                                                                              FILING DATE:
                            LENGTH:
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               amino acid
                             480 amino acids
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Two Embarcadero Center, 8th Floor
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Tsuchihashi, Zen
Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feder, John N.
Kronmal, Gregory
Lauer, Peter M.
Ruddy, David A.
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not relevant
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RESULT 3
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COCATION: 1.480
OTHER INFORMATION:
US-08-724-394A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local Similarity
                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                           CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-CCT-1996
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 470 amino acids
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                STRANDEDNESS:
TOPOLOGY: not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 IAPRYSSELMGASRGESSIAPVIVPTVSGELLSQDPEEFGWRNVEELLEAVNLLGLLEYLI 383
                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           463 FGEADVQEWAKERKLTRL 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                       San Francisco
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                                                                                                               415-576-0300
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               not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kronmal, Gregory S.
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                                                                                                                             415-576-0200
                                                                                                                                                                                                                                         01-OCT-1996
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Sequences and Antibodies Thereto
31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.4%; Score 138; DB 2; Lx 100.0%; Pred. No. 5.5e-123; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "NPT4"
                                                                                                                                                                       35,136
                                                                                                                                                           017957-000100
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US-08-363-586-1

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Best Local Similarity
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                                                                                                                          ; MOLECULE TYPE: US-08-934-915-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 47, Appli
Patent No. 5932412
GENERAL INFORMATI
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                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
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11
                           56 QLNDSSE 62
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                     TELEFAX: 813-538-3820
QLNDSSE 17
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                                                                                                                                                              amino acid
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17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                             20 amino acids
                                                      Conservative
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                                                                                                                                      peptide
                                               1.7%; >cc
100.0%; Pr
0;
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                                                   Score 7; DB 2; Pred. No. 4.9
0; Mismatches
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Pred. No.
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Query Match
Best Local Similarity
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PCT-US94-05150-22
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                                                                                                                                                                        Sequence 22, Application PC/TUS9405150 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-JUL-1192
APPLICATION NUMBER: EP 91111720.8
FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
             SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         APPLICANT:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3315
APPLICATION NUMBER:
                                          COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                      22 QLNDSSE 28
                                                                                                                                                                                                                                                                                                56 QLNDSSE 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wadler, Linda A. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 23-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                          1.7%; United 100.0%; Pr/0;
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Peptides for the
                                                                                                                         Purified Mammalian Flt3 Ligands and
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PCT/US94/05150
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Pred. No.
                                            6.0.5
                                                                                                                                                                                                                                                                                                                                  Mismatches
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Diagnostic Purpose
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US-08-406-248-6
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INFORMATION FOR SEQUENCE CHARACTERISTICS:
FRIGHH: 57 mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08406248
Patent No. 5736318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
                                         ATTORNEY/AGENT INFORMATION:
NAME: MCDENTIELS, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET UNMBER: HAZ-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
STREET: 200 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING TITLE OF INVENTION: TRANSFORMED CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01 FILING DATE: 07-JUL-1993 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
US 08/089, 263
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APPLICATION NUMBER: US 08/092,549
FILING DATE: 16-JUL-1993
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APPLICATION NUMBER: US 08/11/, 321
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/106,340
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                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 02109
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TOPOLOGY: linear
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CHARACTERISTICS:
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03-DEC-1993
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                                 Query Match
Best Local Similarity iou.
""+ches 7; Conservative
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Best Local Similarity
""+" 7; Conserve
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-248-6
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Patent No. 58
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 20:
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                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acid
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/00 FILING DATE: 02-JUN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSeq 2.0
CURRENT APPLICATION DATA:
182 QLNDSSE 188
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Damle, Nitin K APPLICANT: Brady, William
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                         56 QLNDSSE 62
                                                                                                                                                                                                                                                                                  NAME: Adriano, Sarah B. REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                    TYPE: amino acid
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27 QLNDSSE 33
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CITY: Los Angeles
STATE: California
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100.0%; Pr
                                                                   100.0%;
                                                                  1.7%; Score 7; I
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%; Pred. No. 22;
0; Mismatches
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                                                    Mismatches
                                                                  DB 2;
o. 52;
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o. 22;
                                                                              Length 253;
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RESULT 9 US-08-889-666-20 ; Sequence 20, Application US/08889666 ; Patent No. 5885579

SENERAL INFORMATION:

Ledbetter,

Jeffrey

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Linsley, Peter S.

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Best Local S
Matches 7
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                                                                                                                                                                                                                                  Patent No. 5885796
GENERAL INFORMATION:
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                                                                                                  APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                  APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey
APPLICANT: Danle, Nitin K.
APPLICANT: Brady, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 F
COUNTRY: UL. 90025
                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                     182 QLNDSSE 188
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                                                                                                                                                                                                                                                                                                                                                                                   56 QLNDSSE 62
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REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 0 FILING DATE: 18-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                        CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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5885796
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                                                                   E: Merchant & Gould
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Brady, William
                       USA
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tive 0; Mismatches
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5. 52;
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Best Local Similarity
Matches 7; Conserve
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US-08-725-776-20
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Patent No. 5968510
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FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adilano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310.445-1140
         CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REGISTRATION NUMBER: 34,470
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                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Brady, William APPLICANT: Kiener, Peter TITLE OF INVENTION: CTLA4
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PRIOR APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       CITY: Los Angeles
STATE: California
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                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 QLNDSSE 62
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 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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WENTION: CTLA4 Receptor
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100.0%; Pred. No. 52;
ative 0; Mismatches
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30436-35US01
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                                                                                                                                                                                                                                                                                                                                                            Suite 400
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Query Match
Best Local Similarity
7; Conserve
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US-08-488-062-20
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Best Local Similarity luv.
Thes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                        TELEFAX: 310-445-9031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Linsle
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TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 20:
                                                                                                  MOLECULE TYPE:
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                           NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                TOPOLOGY:
                                                                                                                            STRANDEDNESS
                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/375390 FILING DATE: 18-JAN-1995
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 253 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ledbetter, Jeffre Damle, Nitin K. Brady, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08488062
             Conservative
                                                                                                                                                                                                 310-445-9031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linsley, Peter S.
Ledbetter, Jeffrey A.
                                                                                                                                                                                                                 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merchant & Gould
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                         100.0%;
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100.0%; Pred. No. 52,
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       US/08/488,062
       ; Score 7; DB 2
%; Pred. No. 52;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
                        DB 2;
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         0;
                                  Length 253;
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       Indels
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   0;
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US-08-805-118-3; Sequence 3, Application US/08805118; Patent No. 5985604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compaction.

COMPUTER: IBM PC compaction.

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/117,083

FILING DATE: 10-SEP-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Dreger, Walter H.

REGISTRATION NUMBER: 24,190

REFERENCE/DOCKET NUMBER: A-58783

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-398-3249

TELEFAX: 415-398-3249
                                                                                                                          밁
                                                                     RESULT 14
                                                                                                                                                                                                                                                                               US-08-117-083-9
                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-729
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
FRIGTH: 263 amino acids
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US-08-117-083-9
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Best Local Similarity

Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                     188 QLNDSSE 194
                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
LOCATION: 1..263
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Boursnell, Michael APPLICANT: Inglis, Stephen C. APPLICANT: Munro, Alan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
                                                                                                                                         56 QLNDSSE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single TOPOLOGY: linear
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CITY: San Francisco
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100.0%; Pred. No. 54;
tive 0; Mismatches
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GENERAL INFORMATION:

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APPLICANT: Lal, Preeti APPLICANT: Bandman, Olga TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT

TITLE OF INVENTION: PH NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS:

PHOSPHATE CO-TRANSPORTER

CITY: Palo Alto

S

ADDRESSEE:

E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive

COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

94304

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US-08-724-394A-9
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Feder,
APPLICANT: Kronmal
APPLICANT: Lauer,
                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08724394A Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                           APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston
APPLICANT: Thomas, Winston
APPLICANT: Touchihashi, Zenta
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: NO.
TITLE OF INVENTION: Sequences and Antibodies There
NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:
ADDRESSEE: TWO Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATFORNEY_AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERREZ_POCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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LIBRARY: GenBank
CLONE: 450532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/805,118
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                    Lauer, Peter M.
                                                                                                                                                                                                                                                                                     Feder, John N.
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100.0%; Pr
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Search completed: May 25, 2000, 14:54:52 Job time: 1654 sec
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                                                                                                                                               Query Match 1. Best Local Similarity 100 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                 401 LDIAPRY 407
                                                                                                                322 LDIAPRY 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/01 FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                       480 amino acids
                                                                                                                                                                                                                                                                                 Region
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Page 8

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9b_p12: CNS019DX
9b_p12: CCPCNAM
9b_p12: AF202292
9b_p11: NTA18135
9b_p11: RSPCNA
9b_p11: RSPCNA
9b_p11: RSPCNA
9b_p11: RSPCNA
9b_p11: CCBTUB1A
9b_p11: CCBTUB1A
9b_p23: HSU90544
9b_p11: CCBTUB1B
9b_p3: HSU90544
9b_p11: CCBTUB1B
9b_p11: CCBTUB1B
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9b_p11: CRBTUB1B
9b_p11: RP0106665
9b_p11: RP0106665
9b_p11: AF015775
9b_p2: AF015775
9b_p2: AF005665
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9b_p71: AP001063
9b_p71: AP001063
9b_htg2: AC003656_1
9b_htg2: AC003656_1
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9b_htg3: AC0101714
9b_htg3: AC010676
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gb_pr3: HSU90545
gb_pr2: HSZ83953
gb_htg2: AL138726
gb_htg4: AC012145
gb_htg3: AF182108
gb_pl2: CNS019DX
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Database length: -486395729
Search time (sec): 737.360000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
Query: US-09-391-958-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -MODEL-frame+_P2n.model -DEV=xlp
-Q=/Ggn2_1/USPTO_spool/US9391558/runat_24052000_213605_8839/app_query.fasta.1
-Q=/Ggn2_1/USPTO_spool/US9391558/runat_24052000_213605_8839/app_query.fasta.1
-DB=-GenEmbl -QFNT=fastap -SUFFIX=oligo.rge -GAPOD=4.500
-GAPEXT=0.050 -MINANCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPEXT=0.050 -VGAPOD=60.000 -YGAPEXT=60.000
-FGAPEXT=7.000 -YGAPOD=60.000 -YGAPEXT=60.000
-DELOP=6.000 -EGAPEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US09391958 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000 XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      мау
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Compugen Ltd
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71 y 18135 Nicotiana tabacum mRNA for
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1 AR036571 Sequence 19 from pate
1 U90545 Human sodium phosphate
U90544 Human sodium phosphate | X71785 C.crispus gene for beta | X72588 H.morrhuae ribosomal | AC016964 Homo sapiens clone | AF040644 Caenorhabditis elega | AF015775 Bacillus subtilis | YC | AF006665 Bacillus subtilis | YC | AF001602 Homo sapiens genomic | Z75543 Caenorhabditis elegan | AF0125448 Caenorhabditis elegan | AF0125448 Caenorhabditis elegan | AF0125448 Caenorhabditis elegan | AF025431 Human DAN sequence | AC015270 Drosophila melanogas | Continuation (2 of 8) of ACC | Continuation (3 of 8) of ACC | AL021531 Human DAN sequence | AC010141 Homo sapiens chromo | AC010376 Homo sapiens chromo | AC010714 Drosophila melanoga | AC006876 Caenorhabditis elegan | AC006876 Caenorhabditis elegan | X82899 Human DNA sequence | F
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AB010965 Haloarcula sp. gene f
D63786 Haloarcula mtrapanicum I
X00662 Haloarcus morrhua 16S
X71784 C.orispus mRNA for beta
L11333 Mouse carboxyesterase m
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9b_htg1:HSJ181N11
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Sequence 19 from patent
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Feder, J.Nathan, Kronmal, G.Scott, Lauer, P.M., Tsuchihashi, Z. and Wolff, R.K.
Megabase transcript map: novel sequences and Patent: US 5872237-A 19 16-FEB-1999;
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I ALI38726 Homo sapiens chr
I ACO10575 Drosophila melan
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                                                                                                                                                                                                                                                                                                                                                                                                   Ruddy,D.A., Kronmal,G.S., Lee,Y.K., Mintler,G.A., Quintana,L., Domingo,R. Jr., Meyer,N.C., Basava,A., McClelland,B., Fullan,A., Maga,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C., Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J.N.
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JOURNAL REFERENCE AUTHORS

TITLE

FEATURES

gene CDS

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

ORGANISM

seq_name:

1507

394

1457

361

1357

344

1307

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alignment_block:
US-09-391-958-1 x HSU90545
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: HSU90545
                                                                                                                                                                                                                                        211 TrpLeuValSerThrMetValValTyrIleProThrTyrIleSerSerVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yLeuLeuPheTyrLeuIlePheGlyGluAlaAspValGlnGluTrpAlaL 394
                                    CTGTCATTGTACCCACTGTCAGCGGATTTCTTCTTAGTCAGGACCCTGAG
                                                                                                  roVallleValProThrValSerGlyPheLeuLeuSerGlnAspProGlu
                                                                                                                                      ThrLeuCysGlnSerGlyIleTyrIleAsnValLeuAspIleAlaProAr
                                                                                                                                                                                                                                                                                          ACATTGTGTCAGTCAGGGATTTATATCAATGTCTTAGATATTGCTCCAAG
                                                                                                                                                                                                                                                                                                                                                          LeuThrLysLysPheArgLeuIleThrValArgLysIleAlaThrIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAACCAAAAGTTTAGACTCATCACTGTGAGGAAAATTGCCACAATTTT
                                                                                                                                                                                                                                                                                                                                                                                             TTGTTGCCTGGGTCATAGGCATGGTGGGAGGCTATCTGGCAGATTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 leValAlaTrpValIleGlyMetValGlyGlyTyTLeuAlaAspPheLeu
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Ratio:
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LGSLPSSALIVSLPYLNSGYITARALLTLSCGLSTLCOSGIYINVLDIAPRYSSFLMG
ASRGFSSIAPPIIVPTVSGFLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIFGEADVQEW
AKERKLTRL"
436 c 402 g 484 t
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Gaps: 0
Identity: 100.000
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alignment_block:
US-09-391-958-1 x HSZ83953
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AUTHORS
TITLE
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AUTHORS
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ORGANISM
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ORIGIN
 seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 98.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                        146 ValCysCysLeuLeuTrpPheValValIleTyrAspAspProValSerTy 162
                                                                                                                                                                                                                      129 luThrLeuGlyTrpProPheValPheTyrIlePheGlyGlyValGlyCys 145
                                                                                                                                                                                                                                                                                112 yMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSerG 129
                                                           179
                                                                                                                                                                                                                                                                                                                          276 TGGGGCCCTCCACAAGAACGAAGCAGACTCTGCAGCATTGCTTTATCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                        96 TrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSerGl 112
                              rProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLysG 179
                                                                                                                                               AATGTTACTGGGATGCTTTACTGCCATCCTCATAGGTGGCTTCATTAGTG
                                                                                                                                                                                                        AAACCCTTGGGTGGCCCTTTGTCTTCTATATCTTTGGAGGTGTTGGCTGT
gb_htg2:AL138726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-JAN-1997) Gasparini P., Servizio di Genetica Medica, I.R.C.C.S. - Ospedale CSS Viale Cappuccini, I-71013 San Giovanni Rotondo, Foggia, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 570)
Gasparini, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z83953.1 GI:1783342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 570)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="CD 274"
134 c 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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Gaps:
Percent Identity:
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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US-09-391-958-1 x AL138726/rev
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Quality:
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LOCUS AL138726 1
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                                                                                                                                                                                                                                                                                                            Quality: 71.00
Ratio: 1.000
Percent Similarity: 100.000
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TITLE
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                                                                             source
28 eCysAsnPheThrThrIleAlaGlnAsnValIleMetAsnIleThrMetV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 16, 2000 this sequence version replaced gi:6911804.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00749 Length: 9637bp Contig_ID: 00749 Length: 9637bp Contig_ID: 01824 Length: 9637bp Contig_ID: 01824 Length: 15932bp.
* NOTE: This is a 'working draft' sequence. It currently a consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.

20679: contig of 20679 bp in length
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20679: contig of 20679 bp in length
20680 21479: gap of 800 bp
21480 84894: contig of 63415 bp in length
84895 85694: gap of 800 bp
85695 95331: contig of 9637 bp in length
95332 96131: gap of 800 bp
96132 123534: contig of 27403 bp in length
123535 124334: gap of 800 bp
124335 140266: contig of 15932 bp in length.
Location/Qualifiers
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/clone="RP1-1"
/clone=1b="RPC1-1"
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a 26597 c 25588 g 42968
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                                                                               65594
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EQUENCING IN
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REFERENCE
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RS Birren, B., Linton, L., Neckerly, R., BoguslavKiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., BoguslavKiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Cocke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meddrim, J., McDrow, J., Naylor, J., Norman, C., H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Tstaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wynan, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rLeuProAlaLys 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (20-OCT-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 19, 1999 this sequence version replaced gi:6087932. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149155)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-11K15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                         NOTE: This is a 'working draft' sequence. It current consists of 13 contigs. The true order of the pieces
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                                                                                                    Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 108943 bases at least Q40 Consensus quality: 127281 bases at least Q30 Consensus quality: 140888 bases at least Q20 Insert size: 149155; sum-of-contigs Quality coverage: 4.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L3182
Center clone name: 11_K_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submission@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR
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RP11-11K15, WORKING DRAFT SEQUENCE, 13 uno
                                                        It currently
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AUTHORS
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ORGANISM
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US-09-391-958-1 x AC012145
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LOCUS AF182108 1
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                     JOURNAL
                                              TITLE
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                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 167065)
Schudy.A., Schilhabel.M., Baumgart,C., Menzel,U., Weber,J., Schattevoy.R. and Rosenthal,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Submitted (31-AUG-1999) Genome Analysis, Institute of Molecular
                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                          AF182108 167065 bp
Homo sapiens chromosome
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1
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* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45294 a
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/db_xref="taxon:9606"
/clone="RFP11-11K15"
/clone_lib="RPCI-11 Human M.
a 30075 c 29603 g 44177 t
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45513: contig of 16233 bp in length
61680: contig of 16167 bp in length
76539: contig of 14859 bp in length
gap of unknown length
gap of unknown length
96748: contig of 20209 bp in length
gap of unknown length
122261: contig of 25513 bp in length
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149155: contig of 26894 bp in
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gap of unknown 1
3309: contig of 1382 b
gap of unknown 1
4771: contig of 1462 b
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Gaps: 0
Percent Identity: 100.000
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exon complement(40834267) /note="GENSCAN"	repeat_region	repeat_region 37613841 /rpt_family="11m45"	•	exon complement(36923753)	repeat_region 36023612. in 15/15/15/15/15/15/15/15/15/15/15/15/15/1	repeat_region 32953436	repeat_region complement(31934453) /rpt_family="L1MEC_5end"	_regron		<pre>/rpt_family="11m35" repeat_region 29753140</pre>	repeat_region 2948 .3013	repeat_region complement(29163181)	repeat_region 2006, 3016	repeat_region 29043033 /rot_familv="11m45"		repeat_region complement(27792805)	repeat_region 27792806	repeat_region complement(21482195) /rpt_family="11ma5"	/rpt_family="llmas	<pre>/rpt_family="llma2" repeat region complement/2148 2195)</pre>	repeat_region complement(20912154)	repeat_region 20802210	repeat_region 20792156	repeat_region complement(20772161) /rot family="llma5"	repeat_region 17511824 /note="SST_REPEAT"		exon 1704. 1779	repeat_region 8821153	L (0	exon 746770	repeat_region 514. 546	/clone="BAC R-11N9"	/chromosome="8"	/or	FEATURES Location/Qualifiers source 1167065	+ be	* This record will be updated with the finished sequence	<pre>size. * NOTE: This is a 'working draft' sequence.</pre>	- 154345 contig 8: pos. 154346 - 167062 Inbetween gaps of unknown	pos. 48338 - 65090 contig 4: pos. 65091 - 92971 contig 5: pos	Ι.
ָר בַּי	repeat region	+	repeat_region	repeat_region	repeat_region		exon	exon		exon	repeat_region	repeac_regroun	, ,	+	repeat_region	repeat_region	repeat_region	repeat_region	uor 6ar_redar	+	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	uorfar_redau	-	D 400	exon		repeat_region	repeat_region	repeat_region		repeat region	repeat_region	repeat_region	repeat_region	repeat_region		exon
/note="SST_REPEAT" 66396675	/note="XNUN_REPEAT" 66306698	<pre>/note="SST_REPEAT" 6624 6698</pre>	/note="SST_REPEAT" 66246658	/note="SST_REPEAT" 66246686		note="MZEF"	/evidence-not_experimental complement(6425,6488)	<pre>complement(61766336) /note="GRAIL"</pre>	/evidence=not_experimental	ent(852	/note="SST_REPEAT"	Sign	/note="XNUN_REPEAT"	/rpt_tamily="sva" 55295562	.5512	5405	53885461 /rpt family="alu"	/rpt_family="sva"	/rpt_family="sva"	/rpt_family="sva" 52595319	/rpt_ramity="alu" 52585380	5255 . 5540	52515553	52515540 /rpt_family="ALU"	/rpt_family="alu"	CAN"	/evidence=not_experimental	<pre>complement(45744701) /note="MZEF"</pre>	<pre>/note="(TA)n" /rpt_family="Simple_repeat"</pre>	complement (44964536)	/note="SST REDEAT"	D.,		/rpt_type=tandem	/IIOCE="SST_REFEAT" 44784533	4477. 4534		44614558 /note="XNUN_REPEAT"	/note="MZEF" /evidence=not_experimental	complement(43114354)

exon

exon

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seq_name: gb_pl2:CNS019Dx
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Ratio: 1.000
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              Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr. 78026 Versailles, France 2 (bases 1 to 660)
                                                                        Eukaryota; Fungi; Ascomycota; Euascomycetes; Discomycetes; Leotiales; Sclerotiniaceae; Botryotinia.

1 (bases 1 to 660)

Bitton, F., Levis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Direct Submission
                                                                                                                                                          cDNA library; nitrogen deprivation
Botryotinia fuckeliana
Botryotinia fuckeliana
                                                                                                                                                                                                                                      Botrytis cinerea strain nitrogen deprivation. AL111517
                                                                                                                                                                                                                 AL111517.1 GI:5826136
                                                                                                                                                                                                                                                                                          CNS019DX
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/rpt_family="ALU"
complement(9126. .9287)
/rpt_family="alu"
complement(9136. .9195)
/rpt_family="sya"
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complement(9080...9
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complement(8687..8767)
/rpt_family="l1pa7"
complement(8787..9554)
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complement(8683..87
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3684. .8768
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/rpt_family="llpa11"
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complement(8489. .8518)
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complement(7342...7506)
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3446. RECO
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6727. .6814
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US-09-391-958-1 x CNS019DX
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Direct Submission

Direct Submission

Direct Submission

Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :

CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)

The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
                                                                                                                                                                                       Submitted (23-OCT-1991) S.Hata, Faculty of Science, Himeji
Institute of Technology, Kamigori, Ako-gun, Hyogo 678-12, Location/Qualifiers
                                                                                                                                                                                                                                               Hata, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                              Identification of carrot cDNA clones encoding a second putative proliferating cell-nuclear antigen, DNA polymerase delta auxiliary
                                                                                                                                                                                                                                                                                                                                                                                                  Hata, S., Kouchi, H., Tanaka, Y., Minami, E., Matsumoto, T., Suzuka, I.
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

1 (bases I to 865)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferating cell nuclear antigen.
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     9.00
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                                                                                                       /db_xref="taxon:4039"
168 c 222 g
                                                                                                                                             /organism="Daucus carota"
/cultivar="Kurodagosun"
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/strain="T4"
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REFERENCE AUTHORS TITLE

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KEYWORDS SOURCE ORGANISM ACCESSION VERSION

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US-09-391-958-1 x AF202292/rev
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Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; Solananae; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 922)
Duong van, H., Gaikwad, A.S. and Mukherjee, S.
                                                                                                                                                   Nicotiana tabacum
Y18135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vandenkoornhuyse, P., Martel, M.H. and Leyval, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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1 (bases 1 to 870)
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175 c 241 g 218 t
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/strain="cl 3-10"
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Shimizu,S. and Mor1,H.

Analysis of cycles of dormancy and growth in pea axillary buds based on mRNA accumulation patterns of cell cycle-related gene
                                                                                             Direct Submission
Submitted (17-0CT-1997) to the DDBJ/EMBL/GenBank databases. Hitoshi Mori, Nagoya University, School of Agricultural Sciences; Furo-cho Chikusa-ku, Nagoya, Aichi 464-01, Japan (E-mail:morihito@nuagrl.agr.nagoya-u.ac.jp, Tel:052-789-4167,
                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; Rosidae; Fabales; Fabaceae; Papillonoideae; Pisum.

1 (bases 1 to 948)
Shimizu, S. and Mori, H.
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Pisum sativum mRNA
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Submitted (23-SEP-1998) S. Mukherjee, International Center For Genetic, Engineering And Biotechnology, Plant Molecular Biololgy Lab, Po Box: 10504, Aruna Asaf Ali Marg, New Delhi 110067, INDIA
                                                                                                                                                                                                                                                                                         Pisum sativum cDNA to mRNA.
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FESPTQDKISDFEMKLMDIDSEHLGIPEAEYHAIVRMPSAEFARICKDLSSIGDTVVI
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TPLSSSYTISLSNELPVVVEYKIAEMGYVRFYLAPKIEEDEEETKPQA"
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                                                                                                                                                                                                                                                                                                  Mukherjee, S.
Direct Submission
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1 (bases 1 to 990)
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/db_xref="taxon:3888"
/clone_lib="lambda Uni-Zap"
                                                                                 /gene="PCNA"
12. .812
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/ALVALLILRSBEFEHYRCDRULSMGMULNNMAKMLKCAGNDDIITIKADDGSDTVTFM
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AVSKEGYMFIKGDIGSANIVCRQNTTYDKPBEATYLEMBEPVALOFALRYMNSFTKA
TPLSSSYTISLSNELPYVYEYKIAEMGYVRFYLAPKIEEDEEETKPQA"
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Haloarcula argentinos spec.nov. and Haloarcula mukohatas spec.
nov., Two new species of extreme halophilic archae from argentina
Unpublished (1995)
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Ihara,K., Watanabe,S.
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376 c 472 g
                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Haloarcula vallismortis"
/db_xref="taxon:28442"
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VALVALLLRSEGFEHYRCDRNLSMGMNLNNMAKMLKCAGNDDIITIKADDGSDTVTFM
FESPTODKISDFEMKLMDIDSEHLGIPEAEYHAIVRMPSAEFARICKDLSSIGDTVVI
AVSKEGVKFSTKGDIGSANIVCRQNTTVDKPEEATVIEMNEEVALQFALRYMNSFTKA
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Percent Identity:

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seq_documentation_block:
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ACCESSION D63786
VERSION D63786.1 GI:
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US-09-391-958-1 x D50851/rev
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US-09-391-958-1 x AB010965/rev
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Ratio: 1.000
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                                                                                                                                                                                                                                                        298 ACCGTCTCCGGGTTCTTGCTCTCACAA 272
                                            Halorubrum trapanicum (strain:JCM8979) DNA.
Halorubrum trapanicum
Archaea; Euryarchaeota; Halobacteriales; Ha
                                                                                                                  D63786.1 GI:2315141
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Haloarcula quadrata sp. nov., a square, motile archaeon
from a brine pool in Sinai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haloarcula sp. (strain:801030/1) DNA.
Haloarcula sp.
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                 Halorubrum trapanicum DNA for 16S rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-FEB-1998) to the DDBJ/EMBL/GenBank databases. Masahiro Kamekura, Noda Institute for Scientific Research; 399 Noda, Noda, Chiba 278, Japan (E-mail:mkamekur@supernig.nig.ac.jp, Tel:0471-23-5573, Fax:0471-23-5959)
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Kamekura, M.
Direct Submission
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AB010965.1
I (bases 1 to 1472)
Kamekura, M.
                                                                                                    16S ribosomal RNA
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                                Halorubrum.
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/strain="801030/1"
/db_xref="taxon:44098"
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381 c 476 g
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source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kamekura, M., Dyall-Smith, M.L., Upasani, V., Ventosa, A. and Kates, M. Diversity of alkaliphilic halobacteria: proposals for transfer of Natronobacterium vacuolatum, Natronobacterium myacuolatum, Natronobacterium pharaonis to Halorubrum, Natrialba, and Natronomonas gen. nov., respectively, as Halorubrum vacuolatum comb. nov., Natrialba magadii comb. nov., and Natronomonas pharaonis comb. nov., respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Submitted (06-AUG-1995) to the DDBJ/EMBL/GenBank databases. Submitted (06-AUG-1995) to the DDBJ/EMBL/GenBank databases. Masahiro Kamekura, Noda Institute for Scientific Research: 399 Noda, Noda, Chiba 278, Japan (E-mail:mkamekur@supernig.nig.ac.jp, Tel:0471-23-5573, Fax:0471-23-5959)
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                                                                               reverse of:
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389 c 479 g
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/strain="JCM8979"
/db_xref="taxon:29284"
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N_Geneseq_36:Q49052
N_Geneseq_36:Q49052
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N_Geneseq_36:V26754
N_Geneseq_36:V269355
N_Geneseq_36:Q59355
N_Geneseq_36:Q59355
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N_Geneseq_36:V269466
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N_Geneseq_36:V20250
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Database length: 125096042
Search time (sec): 62.170000
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-Q-/cgn2_1/USP70_spco1/US09391958/runat_24052000_213606_8888/app_query.fasta.1
-DB=N_Geneseq_36 -QFMT-fastap -SUFFIX-oligo.rng -GAPOP=4.500
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-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-FGAPEXT=7.000 -YGAPOP=60.000 -YGAPOX=60.000
-FGAPEXT=7.000 -START=1 -MATRIX-Oligo
-TRANS-human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE-quality
-THR_MIN=1 -ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXXEN=1000000 -USER=US09391958 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
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_Geneseq_36:V43712
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4 | Granulin coding sequence. New
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                                                                                                                                        sequence used in development of Elastase inhibiting peptide DNA 21B4 gene clone pT#13, EcoRI in Nuclectide sequence encoding the EST clone CN532. New polynuclec probe (151) for microbial genes EST clone DY167. New polynuclec probe T18 F1t3 ligand peptide Mouse T118 F1t3 ligand peptide Phosphate starvation-induced pr Human gene signature HUMSS08822 CDNA encoding protein homologou Arabidopsis lysine ketoglutarat EST clone BD222. New polynucled
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AC Sodium-dependent phosy cell signalling disor cell signalling cell signalling disorders of cell signalling ce
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                                                                                                                                                                                                                                                                                                                                                                                                  PT New isolated human sodium-dependent phosphate co:transporter - used PT to develop products for treating e.g. cancers, osteoporosis, PT Alzheimer's disease, diabetes, encephalopathy, myopathy, PT hypocalciuria or hypoglycaemia.

PS Claim 5; Fig 1; 66pp; English.

CC c.g. cancers of the kidney, disorders of decreased phosphate levels, cysteneuria, nephrocalcinosis, english the cysteneuria, nephrocalcinosis, familial composition of composition of cysteneuria conductors of cyling progressive composition, cyling progressive cyling cyling progressive cyling cyling progressive cyling cyling cyling cyling progressive cyling 
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                                       AlaLeuLeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIl 317
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ID V57910;

AC V57910;

PT 21-DEC-1998 (first e
DE Human haemochromatosi:
KW Bovine butyrophilin;
KW Bovine butyrophilin;
KW diagnosis; iron metab
KW BFF4; BFF5; milk prot
CDS TONAY-1998.

FF Key 1377.

FT CDS 77.

F
             PT metabolism

PS Claim 58; Fig 7; 209pp; English.

CC The present invention describes hereditary haemochromatosis gene

CC The present invention describes hereditary haemochromatosis gene. Also described is a

CC method to determine the presence or absence of the common hereditary

CC products from the human haemochromatosis gene. Also described is a

CC method to determine the presence or absence of the common hereditary

CC (a) providing DNA or RNA from the individual; and (b) assessing the

CC DNA or RNA for the presence or absence of a haplotype or genotype where

CC the presence or absence of the haplotype genotype indicates the likely

CC the presence or absence of the haplotype genotype indicates the likely

CC presence of the HFE gene mutation in the genome of the individual. The

CC products for use in the diagnosis and treatment of HFE. The present

CC invention also describes BTF genes, which are homologues of the milk

CC and antagonists of BT function. Also described are: (1) a ROREt gene

CC which can be used to develop products for the study, diagnosis and

CC which are homologues of a type 1 sodium transport gene, and can

CC similarly be used for hypophosphatemia. The present sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:V57910
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09-APR-1998.
30-SEP-1997; U17658.
07-MAY 1997; US-852495.
01-OCT 1996; US-724394.
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Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia; type 1 sodium transport gene; ss.
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Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for the diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hereditary haemochromatosis gene
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21-DEC-1998 (first entry)
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/product= "NTP4"
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of hereditary disorders in iron
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alignment_scores

Percent Similarity:

241.00 1.000 100.000

Percent Identity:

100.000

Length:

Quality: Ratio:

alignment_block: US-09-391-958-1 x V57910

Align seg 1/1

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V57910

from:

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seq_documentation_block:
ID V43712 standard; DNA;
AC V43712;
DT 30-NOV-1998 (first 6
DE Sodium-dependent phos
KW Sodium-dependent phos
                                                                                           seq_name:
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Sodium-dependent phosphate cotransporter coding sequence Sodium-dependent phosphate cotransporter; human; NAPTR; c
                           0-NOV-1998 (first entry)
                                                                                                                                                                                                                        ThrLeuCysGlnSerGlyIleTyrIleAsnValLeuAspIleAlaProAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                      erGlyTyrIleThrAlaThrAlaLeuLeuThrLeuSerCysGlyLeuSer
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        leValAlaTrpValIleGlyMetValGlyGlyTyrLeuAlaAspPheLeu

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                                                                                                                    AAGAGAGAAAACTCACTCGTTTA
                                                                                                                                   ysGluArgLysLeuThrArgLeu 401
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                                                                                         N_Geneseq_36:V43712
                                                    standard; DNA;
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 cancer;
 myopathy;
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seq_documentation_block:
ID V57909 standard; cD
AC V57909;

cDNA; 2281

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seq_name: N_Geneseq_36:V57909
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US-09-391-958-1 x V43712
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PT New isolated human sodium-dependent phosphate co:transporter - used PT to develop products for treating e.g. cancers, osteoporosis, PT Alzheimer's disease, diabetes, encephalopathy, myopathy, PT Alzheimer's disease, diabetes, encephalopathy, myopathy, PT Alzheimer's disease, diabetes, encephalopathy, myopathy, PT Nypocalciuria or hypoglycaemia.

PT hypocalciuria or hypoglycaemia.

PT hypocalciuria or hypoglycaemia.

PT Stample V; Page 47; 66pp; English.

CC This sequence represents a fragment of the DNA encoding the human conditions of it can be used to treat or prevent disorders associated conditions of it can be used to treat or prevent disorders associated conditions of it can be used to treat or prevent disorders of concersorosis, familial hypophosphateemia, rickets, cysteneuria, consteoporosis, familial hypophosphateamia, rickets, cysteneuria, consteoporosis, familial hypophosphateamia, rickets, cysteneuria, consteoporosis, familial hypophosphateamia, rickets, cysteneuria, consteoporosis, diabetes mellitus, hereditary amyloidosis, myopathies including consteoporosis, diabetes mellitus, hereditary amyloidosis, myopathies including consteoporosis, encephalopathy, cardiomyopathy, hypokalaemia, Goodpastures considered external ophthalmoplegia, Kearns-Sayre syndrome, myoclonic consteoporosis, and disorders of cell signalling through cAMP, ATP, NADPH and conditional phosphate. Antagonists or inhibitors of NAPTR may be considered to a subject to treat or prevent disorders associated with correcased phosphate levels, e.g. hypocalciuria, hypocalcaemia, and constant of the products can also be used for detection, diagnosis and drug correcation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cell signalling disorder; phosphate regulation disorder; therapy; ss. Homo sapiens. W09837198-A1. W09837198-A1. 27-AUG-1998. 24-FEB-1998; U03745. 24-FEB-1997; US-805118.
                                                                                                                                                                                                                                                                                             101
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                                         251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        screening.
                                                                                                                                                                                                                                                                                                                                                                              51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ATTTATATCAATGTCTTAGATATTGCTCCAAGGTATTCCAGTTTTCTCAT
                                                               rgLeu
                                                                                                                                           ePheGlyGluAlaAspValGlnGluTrpAlaLysGluArgLysLeuThrA
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                                                                                                                            TTCTTCTTGCTGTTTGCCGTTAACCTGTTAGGACTACTCTTCTACCTCAT
                                                                                                                                                                                                                                                                                           TCAGTGGATTTCTTAGTCAGGACCCTGAGTTTGGGTGGAGGAATGTC
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Percent Identity:
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Ratio: 1.000
Percent Similarity: 100.000
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                                   Hereditary haemochromatosis subregion from an unaffected individual. Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; Roret; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemitype 1 sodium transport gene; ss.
                                                                                                                                                                                                                                                                                                       documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the

DNA or RNA for the presence or absence of a haplotype or genotype where
the presence or absence of the haplotype genotype indicates the likely
presence of the HFE gene mutation in the genome of the individual. The
products for use in the diagnosis and treatment of HFE. The present
invention also describes BTF genes, which are homologues of the milk
protein butyrophilin (BT), and can be used in the production of agonists
which can be used to develop products for the study, diagnosis and
treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes
which are homologues of a type 1 sodium transport gene, and can
                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 GlyCysValCysCysLeuLeuTrpPhe 152
                                                                                                                                                                                                   23-DEC-1998 (first entry)
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01-OCT-1996; US-724394.
(PROG-) PROGENTIOR INC.
Feder JN, Kronmal GS, Lauer PM, Ruddy DA, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          products from the human haemochromatosis gene. Also described is a method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 52; Fig 7; 209pp; English.
The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsuchihashi Z, Wolff RK; WPI; 98-240014/21.
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Homo sapiens.
Location/Qual
CDS 419. 1729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-SEP-1997; U17658
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                                                                                                                                                                                                                                                                                                                                                                                                                          GGCTGTGTCTGCTGTCTCCTATGGTTC
                         sapiens.
                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used for hypophosphatemia. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2281 BP;
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                                                                                                                                                                                                                                                                       DNA; 235033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 419. .1729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  624 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Gaps:
Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 μ
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                                                                                                                                                                                                                                                                                                                                                                                                                          1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ţ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
                                                                      hypophosphatemia;
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AC DIT AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-391-958-1 x V57926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC (a) providing DNA or RNA from the individual; and (b) assessing the CC DNA or RNA for the presence or absence of a haplotype or genotype where CC presence or the presence of the haplotype or genotype where CC presence of the HFE gene mutation in the genome of the Inkely CC HFE gene sequences from the present invention can be used to develop CC products for use in the diagnosis and treatment of HFE. The present CC invention also describes BTF genes, which are homologues of the milk CC protein butyrophilin (BT), and can be used to develop cc and antagonists of BT function. Also described are: (1) a RoRet gene CC which can be used to develop products for the study, diagnosis and complete treatment of inpus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can be used for hypophosphatemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217150
                                                                                                                                              09-APR 1998.

30-SEP-1997; U17658.

07-MX-1997; US-552495.

01-CCT-1996; US-724394.

(PROG-) PROGENTIOR INC.
Feder JN, Kronmal GS, Lauer PM, R.
TSUChihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block:
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30-SEP-1997; U17658.
07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
(PROG-) PROGENTIOR INC.
                                      metabolism
                                                                                                                                                                                                                                                                                                                                                                   type 1 sodium transport gene;
Homo sapiens.
W09814466-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Hereditary haemochromatosis subregion from an HH affected individual. Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia
                                                      for the diagnosis and treatment of hereditary disorders in iron
                                                                                       Hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V57903 standard; DNA; 237326 BP V57903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 GlyCysValCysCysLeuLeuTrpPhe 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 8; 209pp; English.
The present invention describes hereditary haemochromatosis gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Feder JN, Kronmal GS, La
Tsuchihashi Z, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism
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for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 98-240014/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGTGTCTGCTGTCTCCTATGGTTC 217176
                                                                                                                             98-240014/21.
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Fig 9; 209pp; English
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1.000
100.000
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BP; 68786 A; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 235033
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                              Ruddy DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e products - used to develop products of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruddy DA,
                                                   hereditary disorders in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48466
                                                                                                                                                                              Thomas WJ
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present invention describes hereditary haemochromatosis gene

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PT hypocalciuria or hypoglycaemia.

PS Example V; Page 36; 66pp; English.

CC This sequence represents a PCR primer for the DNA encoding the human CC sodium-dependent phosphate cotransporter (NAPTR) of the invention. NAPTR CC and agonists of it can be used to treat or prevent disorders associated CC with decreased phosphate levels, e.g. cancers of the kidney, disorders of CC decreased phosphate levels including tumoural calcinosis, osteomalacia, CC osteoporosis, familial hypophosphatemia, rickets, cysteneuria, CC nephrocalcinosis, glomerulonephritis, renal calculus, Alzhelmer's CC disease, diabetes mellitus, hereditary amyloidosis, myopathies including progressive external ophthalmoplegia, Kearns-Sayre syndrome, myoclonic CC epilepsy, encephalopathy, cardiomyopathy, hypokalaemia, Goodpastures cc syndrome, and disorders of cell signalling through cAMP, ATP, NADPH and CC glucose-6-phosphate. Antagonists or inhibitors of NAPTR may be CC administered to a subject to treat or prevent disorders associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-391-958-1 x V57903
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(C) (a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BFF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BF function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can consider the study be used for hypophosphatemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 GlyCysValCysCysLeuLeuTrpPhe 152
                                                                                                                                                                                                                                                                                                                                                                                                              New isolated human sodium-dependent phosphate co:transporter to develop products for treating e.g. cancers, osteoporosis, Alzheimer's disease, diabetes, encephalopathy, myopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bandman O, Lal P;
WPI; 98-467561/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-1998; U03745.
24-FEB-1997; US-805118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9837198-A1
27-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer for Sodium-dependent phosphate cotransporter coding sequence. Sodium-dependent phosphate cotransporter; human; NAPTR; cancer; myopathy; cell signalling disorder; phosphate regulation disorder; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an hereditary haemochromatosis (HH) affected individual. Also described is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCTGTGTCTGCTGTCTCCTATGGTTC 219443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens.
37198-A1.
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Ratio:
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Gaps:
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alignment_block:
US-09-391-958-1 x V43714
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                                                                                               Pri healing and treat psoriasis

ET-1 and ET-2 were isolated from rat kidneys and their amino acid

ET-1 and ET-2 were isolated from rat kidneys and their amino acid

ET-1 and ET-2 were isolated from rat kidneys and their amino acid

ET-1 and ET-2 were isolated from rat kidneys and their amino acid

ET-2 were isolated from rat ET cDNA (Q14338) was obtd.

Dy screening a rat kidney cDNA library in lambda gt10 with PCR

generated ET probes. These probes were also used to obtain the mouse

ET gene (Q14340) from a mouse T-cell genomic library.

ET DNA was also obtained from human sources (Q14339).

An anti-sense ribonucleic acid molecule complementary to the

indicated fragment in the features is also claimed.

ET-1 is a bifunctional growth regulator, capable of stimulating

the growth of some cell types while inhibitory the growth of others.

ET-2 is functionally similar to ET-1 w.r.t. growth inhibitory

bioactivity. In contrast, however, ET-2 is apparently not capable of

eliciting the growth stimulatory activity characteristic of ET-1 and,

in fact, antagonises this ET-1 activity.

See also Q14338-40, Q14952-53, R14328-9 and R15315-20.

Sequence 1779 BP; 304 A; 578 C; 547 G; 350 T;
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 Percent Similarity:
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        increased phosphate levels, e.g. hypocalciuria, hypocalcaemia, and abnormal phosphate regulation in neurons, gastrointestinal tract a liver. The products can also be used for detection, diagnosis and {\bf i}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1991; U02321.
03-APR-1990; US-504508.
13-MAR-1991; US-083796.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q14339 standard; DNA; 1779
Q14339;
                                                                                                                                                                                                                                                                                                                                                                                                                       New cysteine-rich growth modulating proteins, eas inhibitors of neoplastic cell growth and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; R14326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shoyab M, Plowman GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9115510-A.
17-OCT-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_rna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ET; anti-sense RNA; growth regulation; inhibition; stimulation; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human epithelin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIB
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                  Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "claim 9, page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41. .1819
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Percent Identity:
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alignment_block: US-09-391-958-1 x Q14339

Align seg

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Q14339

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seq_documentation_block:
ID Q56794 standard; DNA; 2124
AC Q56794;
DT 22-APR-1994 (first entry)
DE Granulin coding common.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                 seq_name: N_Geneseq_36:Q56794
                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                          PS Disclosure; Fig 9A, 86pp: English.

C This human cDNA sequence includes a coding region for GP88 (see 20 W85474), an 88 kbg glycoprotein autocrine growth factor and epithilin/granulin precursor that is expressed in a tightly compared to the precursor of the precursor that is expressed and unregulated in highly tumorigenic cells derived from normal cells, and which compared the cells. Inhibition of GP88 expression or action in the tumorigenic cells. Inhibition of GP88 expression or action in the cumorigenic cells results in an inhibition of the tumorigenic cells results in an inhibition of the tumorigenic cells are cust of the overproducing cells. Antagonists to GP88 are used to treat diseases associated with increased expression of GP88 particularly cancer but also viral infections. Fragments of CC GP88 are used to raise specific antibodies (used as antagonists, CC as diagnostic reagents and for delivering toxins or other compounds to GP88 expressing cells) and to screen for antibodies. CC Methods are provided for diagnosing disease, or determining cusceptibility to disease, resulting from altered GP88 activity.

SQ Sequence 2095 BP; 364 A; 681 C; 625 G; 425 T;
                                                                                                                                                                                                                                Align seg 1/1 to: V82825 from:
                                                                                                                                                                                                                                                                       US-09-391-958-1 x V82825
                                                                                                                                                                                                                                                                                                                           Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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22-MAY-1998; U10555.
16-DEC-1997; US-991862.
23-MAY-1997; US-863079.
(SERR/) SERRERO G.
Serrero G;
WPI; 99-045276/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; w85475.
Composition containing antagonist of growth factor GP88 - useful for treating cancer and viral diseases and also for diagnosing disease from altered GP88 expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP88; granulin; epithilin; human; growth factor; autocrine; cancer; viral infection; antagonist; therapy; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-1999 (first entry)
Human GP88 autocrine growth factor cDNA.
GP88; granulin; epithilin; human; growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 ProSerSerAlaLeuIleValSer 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
                                                                                                                                                                                      ProSerSerAlaLeuIleValSer 288
                                                                                                                                                     CCATCCAGTGCCCTGATAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATCCAGTGCCCTGATAGTCAGT 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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seq_name: N_Geneseq_36:Q49052
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    Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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P-PSDB; R48673.

New cystine rich granulin peptide(s) from leucocyte(s) - keratinocyte inhibitors useful topically for wound healin Disclosure; Figure 4C; 53pp; English.

The granulin inhibits keratinocytes and is useful in form for promoting the healing of wounds.

Sequence 2198 BP; 398 A; 708 C; 646 G; 446
                                                                                                                                                                                                                                                                                                                                            _documentation_block:
_Q49052 standard; DN
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08-FEB-1992; CA0089.

03-FEB-1992; US-829233.

(SOLO/) SOLOMON S.

SOLOMON S.

SOLOMON S.

SOLOMON S.

P-PSDB; R48673.
                                                                                                                                     W09315195-A.
05-AUG-1993.
28-FEB-1992; CA0089.
03-FEB-1992; US-829233.
                                                                                                      WPI; 93-32
                                                                                                                         (SOLO/) SOLOMON S.
                                                                                                                                                                                                          /transl_except=
misc_difference 1714. .1716
                                                                                                                                                                                                                                                                                         Granulin coding sequence.
Granulin; keratinocytes; wound healing;
                                                                                                                                                                                                                                                 misc_difference
                                                                                                                                                                                                                                                                                 granulocytes; leucocytes;
                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                      393 CCATCCAGTGCCCTGATAGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                  281 ProSerSerAlaLeuIleValSer 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Cystine rich granulin peptide(s) from leucocyte(s) are keratinocyte inhibitors useful topically for wound healing Disclosure; Figure 4c; 53pp; English. The granulin inhibits keratinocytes and is useful in formulations for promoting the healing of wounds.

Sequence 2124 BP; 383 A; 685 C; 630 G; 426 T;
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                                                                                                                                                                                                                                                                                                                    22-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Granulin; keratinocytes; wound healing; inhibition; peptide; granulocytes; leucocytes; ss.
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                                                                                                  93-320328/40.
                                                                                                                                                                                                                                                                       sapiens.
                                                                                                                                                                                                                                             Location/Qualifiers
1453. .1455
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1640. .1642
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                                                                                                                                                                                                                                                                                                                                             DNA;
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Gaps:
Percent Identity:
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                                                             healing
               446 T;
                                   formulations
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seq_documentation_block:
ID Q70754 standard; DNA;
AC Q70754,
C 270754;
DT 22-MAR-1995 (first e
DE Beta tubulin; gene of
KW Beta tubulin; Acremon
KW co-transformation; bi
OS Acremonium chrysogenu
FH Rey
CO-transformation; bi
OS Acremonium chrysogenu
FH Rey
FT | Jabe

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US-09-391-958-1 x Q49052
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Ratio: 1.000
Percent Similarity: 100.000
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New beta tubulin from Acremonium chrysogenum - and relates DNA, vectors and transformed cells, for co-transformations of a wide range of A. chrysogenum strains with foreign genes Claim 4; Page 9-10; 31pp; German.

Vectors based upon the beta tubulin coding sequence may be used to transform Acremonium chrysogenum, optionally in combination with other vectors to introduce a required foreign gene such as the gene encoding glutaryl acylase, an enzyme involved in cephalosporin biosynthesis. The coding sequence may be used to transform a wide variety of Acremonium chrysogenum strains (wild type and mutants). Unlike known systems, it is not recipient-strain limited. Sequence 2206 BP; 449 A; 740 C; 541 G; 476 T;
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                                                                                                                                                                                                                                                                                                                                                     12-FEB-1993; DE-304312.
(FARH ) HOECHST AG.
Kueck U, Nowak C, Wal
WPI; 94-25686/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta tubulin; Acremonium chrysogenum; transformation; co-transformation; biosynthesis; cephalosporins; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beta tubulin gene of Acremonium chrysogenum
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/label-
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/label= Exon
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US-09-391-958-1 x Q70754
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                                                                                                                                                                                              J05192157-A.
03-AUG-1993.
26-MAY-1992; 133384.
27-MAY-1991; JP-121276.
(TAKE ) TAKEDA CHEM IND L'
WPI; 93-277472/35.
P-PSDB; R40226.
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                   DNA fragment contg. DNA coding mutant beta-tubulin - originate from Acremonium chrysogenum, used as selective marker for transformation of A.chrysogenum Example 5; Fig 4-6; 16pp; Japanese.

The wild-type coding sequence for beta-tubulin was isolated fr Acremonium chrysogenum ATCC 11550 and sequenced (Q48230). Prim CTU-3 and CTU-6 were used to introduce mutations at codon 100 to 11e) and 167 (Phe to Tyr), respectively. Expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
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Q48230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acremonium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta tubulin; mutant; chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acremonium chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlySerLeuProSerSerAlaLeu 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chrysogenum.
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1.000
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/number= 3
1749. .2539
                                                                                                                                                                                                                                                                                                                                           /number= 5
/note= "TAA
nucleotides
(Phe to Tyr), respectively. encoded by these sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= h
/number= 4
2603. .3445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleotides
1299. 1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number-
1461. .14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=
1552. .1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "ATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mumber= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'number=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         675. .1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 1484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                beta-tubulin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e
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                                                                                                                                                                                                                                        LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                           termination codon 2994. .2996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         initiation codon 1287. .1289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
      confers chemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.000
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    originates

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                                                                    Primers
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seq_documentation_block:

AC Q55405 standard; DNA;
AC Q55405 standard; MA;
ET ALBUIN; mutant;
AC CATYSOGENUM beta-tu

ET ALBUIN; mutant;
AC CATYSOGENUM chrysogenum beta-tu

ET ALBUIN; mutant;
AC CATYSOGENUM chrysogenum chrysogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:Q55405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-391-958-1 x Q48230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                             03-AUG-1993.
26-MAY-1992; 133384.
27-MAY-1991; JP-121276.
(TAKE ) TAKEDA CHEM IND I
WPI; 93-277472/35.
from Acremonium chrysogenum, used as selective marker transformation of A.chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cephalosporin; antibiotic production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.chrysogenum beta-tubulin Ile(100) mutant coding sequence. Beta tubulin; mutant; chemical resistance; selective marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance (e.g. to microorganisms. See Sequence 3445 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1994 (first entry)
                                            fragment contg. DNA coding mutant beta-tubulin - originates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTCCCTTCCTCGTCTGCACTT 2383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chrysogenum.
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                                                                                                                                                                                                                                         /note= "TAA
nucleotides
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1.000
100.000
                                                                                                                                                                                                                                                                                                                                  /number= 4
2603. .3445
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "wild-type AAC (Asn) codon at position 1887. .1889 is mutated to ATC (Ile) codon" 2540. .2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1749. .2539
/*tag= g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number= 1
/note= "ATG initiation codon is
nucleotides 1287. .1289"
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/*tag= c
                                                                                                                                                                                                                                                                                          /number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1675. .1748
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1552. .1674
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number= 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 3445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     carbendazim and to ansamitocin) on transformed Q55405 and Q55406 for mutated sequences. 723 A; 1061 C; 892 G; 769 T;
                                                                                                                          LTD
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                                                                                                                                                                                                                                       termination codon is located 2994. .2996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resistance;
uction; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selective marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          located
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 8
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seq_documentation_block:
ID Q55406;
AC Q55406 standard; DNA;
AC Q55406;
DT 22-FEB-1994 (first e
DE A.chrysogenum beta-tu
KW Beta tubulin; mutant;
KW cephalosporin; antibi
OS Acremonium chrysogenum
FT Key
FT | (note
FT | (note)
FT | (note
FT | (note)
FT | (n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:Q55406
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-391-958-1 x Q55405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.chrysogenum beta-tubulin Tyr(167) mutant
Beta tubulin; mutant; chemical resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3 and Example 6; Fig 4-6 and Fig 7; 16pp; Japanese. The wild-type coding sequence for beta-tubulin was isolated from Acremonium chrysogenum ATCC 11550 and sequenced (Q48330). Primers CTU-3 and CTU-6 were used to introduce mutations at codon 100 (Asn to Ile) and 167 (Phe to Tyr), respectively. Expression of the mutant proteins encoded by these sequences confers chemical resistance (e.g. to carbendazim and to ansamitocin) on transformed microorganisms. See also Q55406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                278 GlySerLeuProSerSerAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTCCCTTCCCTCGTCTGCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ţo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chrysogenum
  133384.
JP-121276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                  /number= 3
1749. .2539
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotic production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number= 1
/note= "ATG
nucleotides
1299. .1460
/*tag= b
/number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1461. .1484
/*tag= c
/number= 2
                                                                                                                                                                                                /number= 4
2603. .3445
                                                                                                                                                                                                                                                           /note= "wild-type TTC 2088. .2090 is mutated 2540. .2602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1552..1674

/*tag= e

/number= 3

1675..1748
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/number= 2
                                                                                                                        /number= 5
/note= "TAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Gaps:
Percent Identity: 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
                                                                                              termination codon is located 2994. .2996"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          initiation codon is located 1287. .1289"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285
                                                                                                                                                                                                                                                                                     ype TTC (Phe) codon at position
mutated to TAC (Tyr) codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ċ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     selective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding sequence.
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                                                                     /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:PCT-US95-05616-3 + /cgn2_6/ptodata/1/lna/5A_COMB.seq:US-08-020-245A-3 -/cgn2_6/ptodata/1/lna/5A_COMB.seq:US-08-396-957A-3 -/cgn2_6/ptodata/1/lna/5A_COMB.seq:US-08-265-429A-4 + /cgn2_6/ptodata/1/lna/5A_COMB.seq:US-08-265-429A-4 + /cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:PCT-US93-05640-10 +/cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:PCT-US93-056B-1 -/cgn2_6/ptodata/1/lna/PCTUS_COMB.seq:PCT-US93-056B-1 -/cgn2_6/ptodata/1/lna/SA_COMB.seq:US-07-757-536B-1
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Query length: 401
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/cgn2_6/ptodata/1/1na/5A_COMB.seq:US-07-668-3 + 
/cgn2_6/ptodata/1/1na/5C_COMB.seq:US-08-429-998-3 + 
/cgn2_6/ptodata/1/1na/5D_COMB.seq:US-08-431-333-3 + 
/cgn2_6/ptodata/1/1na/PCTUS_COMB.seq:PCT_US91-02321-
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Database sequences: 230463
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Query: US-09-391-958-1
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-724-394A-19
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-Q-/cgn2_1/USPf0_spco1/US9391958/runat_24052000_213606_8858/app_query.fasta.l
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-GAPOP-4.500 -GAPEXT-0.050 -MINMATCH-0.100 -LOOPEL-0.000
-XGAPOP-6.000 -QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-60.000
-XGAPEXT-60.000 -FGAPOP-6.000 -GAPEXT-7.000 -YGAPOP-60.000
-YGAPEXT-60.000 -DELOP-6.000 -DELEXT-7.000 -START-1
-MATRIX-011go -TRANS-human40.cd1 -LIST-45 -DOCALIGN-200
-THR_SCORE-quality -THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -MINLEN-0 -MAXIE.EN-1000000 -USER-US09391958 -NCPU-6
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                                                                                                                                                                                                                          Align seg 1/1 to: US-08-805-118-2 from: 1 to:
                                                                                                                                                                                                                                                                                                     US-09-391-958-1 x US-08-805-118-2
                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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APPLICANT: Bandman, Olga
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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17 rAlaArgTyrGlyIleAlaLeuValLeuHisPheCysAsnPheThrThrI 34
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CLONE: 754412
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REGISTRATION NUMBER: 30
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3174 Porter Drive
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
536
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 05,136
REFERENCE/DOCKET NUMBER: 0179;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 19;
SEQUENCE CHARACTERISTICS:
LENGTH: 1780 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM FC COMPATIBLE
COMPUTER: TEM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
DECEMBER OF PC-DOS/MS-DOS
DECEMBER OF PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: N
TITLE OF INVENTION: Sequences and Antibodies Th
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1435 TTA 1437
                                                               FEATURE:
                                                                                TOPOLOGY: n
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NAME/KEY: misc_feature LOCATION: 1.1780 OTHER INFORMATION: /no
                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9, Application US/08724394A
5872237
                                                                                                  not relevant
not relevant
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                                                                                  CDNA
  /note= "cDNA
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alignment_block:
seq_documentation_block:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                           ysGluArgLysLeuThrArgLeu
                                                                                                                    PheGlyTrpArgAsnValPhePheLeuLeuPheAlaValAsnLeuLeuGl 377
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                                                           AAGAGAAAAACTCACTCGTTTA 1579
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                            /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-805-118-5
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alignment_scores:
Quality:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/80
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
383 ePheGlyGluAlaAspValGlnGluTrpAlaLysGluArgLysLeuThrA 400
                                  151
                                                                 367
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: BRAIT
CLONE: 754412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                 alSerGlyPheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnVal 366
                                                                 PhePheLeuLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIl 383
                                TTCTTCTTGCTGTTTGCCGTTAACCTGTTAGGACTACTCTTCTACCTCAT 200
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US
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Percent Identity: 100.000
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alignment_block:
US-09-391-958-1 x US-08-724-394A-18
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                                                             Align seg 1/1 to: US-08-724-394A-18
                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
1076 GGCTGTGTCTGCTGTCTATGGTTC 1102
                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 415-576-0200
TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                144 GlyCysValCysCysLeuLeuTrpPhe 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: APPLICANT:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                        LOCATION: 1..2266
OTHER INFORMATION:
                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1..2266
                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/OFILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                              1: 2266 base pairs nucleic acid
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                                                                                                                                                            Ratio:
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Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                       not relevant
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Sequences and Antibodies Thereto
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                                                                                                                                     Length: 9
Gaps: 0.
Percent Identity: 100.000
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seq_documentation_block:
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Sequence 21, Application US/08724394A Patent No. 5872237
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                           US-09-391-958-1 x US-08-724-394A-20/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block;
; Sequence 20, Applicati
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                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-OOS
SOSTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
RAGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Megabase Transcript Map: TITLE OF INVENTION: Sequences and Antibodies NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 1..246240 OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Two L. CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ), Application US/08724394A 5872237
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Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lauer, Peter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kronmal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
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                                                                                                                                                                                                                                                                                                                                                                                         /note= "HLA-H.CONTIG"
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                                                                                                                                                                                                                                                            Percent Identity:
                                                                                                                                                                                                                                                                             Length:
Gaps:
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Thereto
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GENERAL INFORMATION:

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alignment_block:
US-09-391-958-1 x US-08-724-394A-21/rev
                                                                                                                                        seq_documentation_block:
                                                                                                                                                                         seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-724-394A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-724-394A-21
                                                                                                                                                                                                                                                                                                                                                                  Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: US-08-724-394A-21
                                                                                                      Sequence 22, Application US/08724394A Patent No. 5872237
                                                                   GENERAL INFORMATION: APPLICANT: Feder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 21:
                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pa
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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   PPLICANT:
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FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fitts, Renee A. REGISTRATION NUMBER: 35,136
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                                                                                                                                                                                                            GGCTGTGTCTGCTGTCTCTATGGTTC 22277
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Tsuchihashi, Zenta
Wolff, Roger K.
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                                                 Feder, John N.
Kronmal, Grego
                Ruddy, David A.
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1..246240
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Winston
                                                 Gregory S
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                                                                                                                                                                                                                                                                                                                                                                   100.000
                                                                                                                                                                                                                                                                              from: 1
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seq_name: /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-805-118-7
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US-09-391-958-1 x US-08-724-394A-22/rev
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   Quality:
                                                                                                                                                                                                                                                            seq_documentation_block:
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                 sequence 7, Application US/08805118 Patent No. 5985604
                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      22303 GGCTGTGTCTGCTGTCTCCTATGGTTC 22277
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                                                                               APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
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CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
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MEDIUM TYPE: Floppy disk
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                               STREET: 3174 POI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
COUNTRY:
                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
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LOCATION: 1..246240
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Wolff, Roger K.
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not relevant
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Sequences and Antibodies Thereto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
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100.000
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OPERATING SYSTEM: MPUTER READABLE FORM: MEDIUM TYPE: Diskett

IBM Compatible DOS

Misrock, S. Leslie

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seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-07-668-648-3
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US-09-391-958-1 x US-08-805-118-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
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US-08-805-118-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/668,648
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                        APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 GlyPheSerSerIleAlaProval 345
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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CLONE: XLF
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LENGTH: 25 base pairs
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/80 FILING DATE: Filed Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                     CLASSIFICATION:
                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                   COUNTRY: U
                                                                                                                                                                                                                                   ADDRESSEE: Pennie a communa Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGATTTTCGAGCATAGCACCTGTC 25
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
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5416192
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alignment_block:
US-09-391-958-1 x US-07-668-648-3
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US-07-668-648-3
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Ratio: 1.000
Percent Similarity: 100.000
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APPLICATION UNMBER: US/08/429,998
FILING DATE: 27-APR-1995
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08429998 Patent No. 5885961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 869-974
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    281 ProserserAlaLeuIleValser 288
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shoyab, Mohammed APPLICANT: Plowman, Gregory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Hom
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                                                                                                                                                                                                                                                                                                                                  STATE: N
                                                                                                                                                                                                                                                                                                                                                                       CITY:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 56:
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                                                                                                                                                                                                                                                                                                                     10036
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                   USA
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Percent Identity:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

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LENGTH:

1779 base pairs

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alignment_block:
US-09-391-958-1 x US-08-429-998-3
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/668,648
FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                 TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                    REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-161-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEPHONE: (212)790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               368 CCATCCAGTGCCCTGATAGTCAGT 391
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ORIGINAL SOURCE:
LENGTH: 1779 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/01 FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1...
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STRANDEDNESS: single
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1155 Avenue of the Americas
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Percent Identity:
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Sequence 3, Application PC/TUS910:
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D
TITLE OF INVENTION: EPITHELIN
TITLE OF INVENTION: MODULATIN
NUMBER OF SEQUENCES: 12
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US-09-391-958-1 x US-08-431-333-3
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Quality:
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; LOCATION:
US-08-431-333-3
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NAME/KEY:
; LOCATION:
PCT-US91-02321-3
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US91/
FILING DATE: 19910403
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                               TELEFAX: (206)448-4775
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiderissue TYPE: Kidney FEATURE:
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: ON TELECOMMUNICATION INFORMATION: TELEPHONE: (206)728-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 ProSerSerAlaLeuIleValSer 288
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ORIGINAL SOURCE:
                                                       FEATURE
                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                      ORGANISM: HOTISSUE TYPE:
                                                                                                                                                 TOPOLOGY:
                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Bristol-Myers Squibb Company STREET: 3005 First Avenue
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                                                                      Homo sapiens
E: Kidney
                                                                                                                                               linear
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Gaps: 0
Percent Identity: 100.000
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alignment_scores:

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alignment_block:
US-09-391-958-1 x US-08-805-118-6/rev
                                                                                                                     alignment_scores:
    Quality:
    Ratio:
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                         Align seg 1/1 to reverse of: US-08-805-118-6
                                                                                                       Percent Similarity:
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US-09-391-958-1 x PCT-US91-02321-3
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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330 SerPheLeuMetGlyAlaSer 336
                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 CCATCCAGTGCCCTGATAGTCAGT 391
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                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 94304
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                                                                                                                                                                                                                                                                                          25 base pairs
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                                                                                                   Percent Identity:
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                                                                                                                    Length:
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; TOPOLOGY: ur; MOLECULE TYPE: PCT-US94-01149-51
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                                                                                          TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51, Application PC/TUS9401149 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 30-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                FILING DATE: 30-AUG-1984
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 2: FILING DATE: 02-NOV-1988 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 64
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 31 FILING DATE: 28-JUL-1989 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            TELEPHONE: 215-270-5096
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TITLE OF INVENTION: Vaccinal Polypeptides
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                             TELEPHONE: 215-270-5090
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                                           STRANDEDNESS:
                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 837,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 1 FILING DATE: 18-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 013,415 FILING DATE: 01-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 1/
FILING DATE: 05-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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Pennsylvania
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                                                           : 41 base pairs
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U.S. Mailcode UW2220 - 709 Swedeland Road
                                 unknown
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             DNA (genomic)
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                                                                                                                                                                                             33,833
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alignment_scores:

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LENGTH: 50 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucl
US-08-325-243A-4
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Quality:
Ratio:
alignment_block:
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US-09-391-958-1 x PCT-US94-01149-51/rev
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Ratio: 1.000
Percent Similarity: 100.000
                                                                                                        Percent Similarity: 100.000
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/325,243A
FILING DATE: 16-DEC-94
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UP 5-31758
FILING DATE: 22-FEB-1993
ATTONEY/AGENT INFORMATION:
NAME: No. 5541288and, Greta E.
REGISTRATION NUMBER: 35,302
PROSENER OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08325243A Patent No. 5541288 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Nishimura, Kaoru
APPLICANT: Okushima, Kinoru
APPLICANT: Okushima, Minoru
APPLICANT: Okushima, Minoru
APPLICANT: Okushima, Minoru
APPLICANT: Okushima, Minoru
APPLICANT: Okushima, Kaoru
APPLICANT: Nishimura, Kaoru
APPLICA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEPAX: 312/474-0448
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STATE: Illlinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tada, Miki
Taoda
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                                                                                                                                                                       7.00
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Gaps: 0
Percent Identity: 100.000
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Gaps: 0
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South Wacker Drive
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Result
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Maximum DB
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Perfect score:
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Match
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Copyright (c) 1993 - 2000 Compugen Ltd
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A;Actessacu. A;Act

aspartate dehydrogenase - Chlamydia pneumoniae (strain CWL029)
(;Species: Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: G72002
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Clinger, L.; Grimwood, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606
A;Accession: G72002

ALIGNMENTS

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A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79580.1; PID:d1043366; PID:gA;Experimental source: strain K1 C;Genetics:
A;Gene: APE0610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: asd
C;Superfamily: yeast aspartate-semialdehyde dehydrogenase
                                                                                                                                                                                          R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                     hypothetical protein APE0610 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: D72647
                                                                                                                                                                                                                                                                                                                                    RESULT
D72647
                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <KAW>
                                                                                                                                   A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A;Reference number: A72450; MUID:99310339
A;Accession: D72647
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8; Conservative
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Query Match

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Length 376;

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RESULT
S35174
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: C75397
R;White, 0; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc
R;White, 0; Eisen, J.Y.; Heidelberg, J.F.; McDonald, L.; Utterback, T.; Zale
S.; Smith, H.O.; Venathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu
A;Reference number: A75250
A;Accession: C75397
A;Accession: C75397
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Best Local Similarity
"atches 7; Conserve
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A;Residues: 1-67 <WHI>
A;Cross-references: GB:AE001987; GB:AE000513; NID:g6459180; PIDN:AAF11003.1; PID:g64591:
A;Experimental source: strain R1
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #
C;Accession: T08424
R;Maleszka, R; de Couet, H.G.; Miklos, G.L.
Proc. Natl. Acad. Sci. U.S.A. 95, 3731-3736, 1998
A;Title: Data transferability from model organisms t
A;Reference number: 216415; MUID:98188272
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-836 <M
A; Cross-references:
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C;Species: Drosophila melanogaster
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
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8; Conservative
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8; Conservative
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ce: strain CantonS
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T.; Zalewski,
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A;Cross-references: GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033 R.Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Volendo J. 9, 153-160, 1990 A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus E; A;Reference number: S12367; MUID:90107938
                                                                                                                                                                                                                              E7 protein - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 20-Aug-1999
C;Accession: A03688; S12367, T10428
                                                                                                        A; Molecule type: DNA
A; Residues: 1-98 <SEE>
                                                                                                                                                             A;Title: Human papillomavirus type 16 DNA sequence A;Reference number: A22355; MUID:85246220
                                                                                                                                               A; Reference number: A22355; A; Accession: A03688
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Virology 145, 181-185, 1985
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A; Genetics:
A; Gene: CESP:D2096.5
A: Thirtnes: 49/3; 84/2
W7WLHS
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A; Accession: T15891
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A;Description: The sequence of C. elegans cosmid D2096
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A;Accession: S35174
A;Accession: S35174
A;Accession: S35174
A;Colecule type: mRNA
A;Residues: 1-68 CMEI>
A;Cross references: EMBL:X69781; NID:9395313; PIDN:CAA49436.1; PID:9395314
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; monooxygenase; c;Z/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A; Residues: 1-97 <GE
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A; Title: Isolation of cytochrome P-450 cDNA clones from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N:Contains: oxidoreductase (EC 1....)
C:Species: Catharanthus roseus (Madagascar periwinkle)
C:Date: 13-Jan-1995 #sequence_revision 09-May-1997 #text_change 11-Jun-1999
C:Accession: S35174
                                                                                                                                                    Best Local Similarity
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                                                                                                                                            1.7%; SC
100.0%; Pr
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100.0%; Pred. No.
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5. 17;
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Vousden,

K.H.

Ela and SV40 l

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A;Accession: S12367
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-98 <BARN
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Tille: A negative element in the human poapillomavirus type 16 genome acts at R;Reference number: Z17014; MUID:91162763
A;Accession: T10428
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033
C;Genetics:
A;Gene: E7
C;Superfemily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif
outer membrane protein homolog - Enterobacter aerogenes plasmid R751 (; Species: Enterobacter aerogenes C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999 C; Accession: T08514 R; Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M. Plasmid 36, 95-111, 1996 A; Title: Conservation of the genetic switch between replication and transfer A; Reference number: Z16434; MUID:97118926 A; Accession: T08514 A; Status: preliminary; translated from GB/EMBI/DDBJ A; Molecule type: DNA
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C; Geneti
A; Gene:
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Best Local Similarity
""" Conserv
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A;Title: Complete sequence and gene organization of the genome of a A;Reference number: A71000; MUID:98344137
A;Accession: E71061
A;Status: preliminary; nucleic acid sequence not shown; translation
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A; Residues: 1-128 <KAW>
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A;Residues: 1-142 <TH
A;Cross-references: E
C;Genetics:
A;Gene: upf30.5
A;Genome: plasmid R75
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
                                       A; Molecule type: DNA
A; Residues: 1-165 <ARN>
                                                                              A;Title: Genome sequence of an obligate intracellular pathogen of A;Reference number: A71570; MUID:99000809
A;Accession: F71505
                                                                                                                                                            A;Cross-references: GB:M80325; NID:g144617; PIDN:AAA23178.1; PID:g144627 A;Note: sequence extracted from NCBI backbone (NCBIN:79464, NCBIP:79474) R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind,
                                                                                                                                                                                                                                                                                                           R;Kaul, R.; Gray, G.J.; Koehncke, N.R.; Gu
J. Bacteriol. 174, 1205-1212, 1992
A;Title: Cloning and sequence analysis of
A;Reference number: A42645; MUID:92138612
                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Chlamydia trachomatis
C;Date: 01-Jan-1993 #sequence_revision 18-Nov-1994
C;Accession: A45192; F71505
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A;Map position: FOR198967-199422
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C;Accession: H64325
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H64325
A;Cross-references: GB:AE001323; GB:AE001273; NID:g3328931; A;Experimental source: serotype D, strain UW-3/Cx
                                                                                                                                          Science 282, 754-759, 1998
                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-165 <KAU>
                                                                                                                                                                                                                                                                                       A; Reference number: A42645;
A; Accession: A45192
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A; Residues: 1-151 <BUL>
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A;Accession: H64325
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                   PIDN: AAC68113.1;
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A;Cross-references: GB:AE000490; GB:U00096; NID:g2367356; PIDN:AAC77142.1; PID:g1790628. A;Experimental source: strain K-12, substrain MG1655
                                                                                                                             Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: D65229
                                                                                                                                                                                                        A;Cross-references: EMBL:U14003; NID:g1263172; PIDN:AAA97081.1; PID:g537026 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; .A.; Rose, D.J.; Mau, S.; Shao, Y.
                                                            A; Molecule type: DNA
A; Residues: 1-212 <BLAT>
                                                                                         A; Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                    R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region A;Reference number: S56314; MUID:95334362
A;Accession: S56410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Escherichia coli
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C;Accession: S56410; D65229
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A;Accession: S75094
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-172 <KAN>
A;Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17956.1; PID:d101868
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein slr0271
                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-212 <BUR>
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A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S75094
C;Accession: S75094
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Pariety: Sato, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
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C;Superfamily: Escherichia coli ribosomal protein
C;Keywords: protein biosynthesis; ribosome
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R;Lyman, S.D.; James, L.; ESCODAI, S.; DUWHEY, H., UN TALLE, TONCOGENE 10, 149-157, 1995
A;Title: Identification of soluble and membrane-bound isoforms of A;Reference number: 158343; MUID:95124710
A;Accession: I58343
A;Accession: I58343
Q
                                                                                     A;Molecule type: mRNA
A;Restidues: 1-220 <RES>
A;Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480
                                                                                                                                                                                                                               C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
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Nature 368, 643-648, 1994
A;Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates
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R;Hannum, C.; Culpepper, J.; Campbell, D.; 1
felt, A.; Muench, M.; Kelner, G.; Namikawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLT3/FLK2 ligand (clone T118) - mouse C;Species: Mus musculus (house mouse) C;Date: 20-Oct-1994 #sequence_revision
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024439 drosophila
P39295 escherichia
P04784 triticum ae
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P19841 homo sapien
P21327 bos taurus
005832 mycobacteri
014916 homo sapien
061983 mus musculu
028722 oryctolagus
062795 rattus norv
P24446 herpes simp
P34644 caenorhabdi
93710 enterococu
P47661 mycoplasma
P53552 saccharomyc
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P24586 schizosacch
P02987 escherichia
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING I
INTO CELLS VIA NA+ COTRANSPORT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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U90544; AAB53422.1;
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C., Tsuchihashi
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EMBL; D00735; BAA00633.1; --
EMBL; U76411; AAB18963.1; --
EMBL; U76412; AAB18963.1; --
EMBL; U76413; AAB18964.1; --
EMBL; AF003020; AAB70737.1; --
EMBL; AF003023; AAB70740.1; --
EMBL; AF003024; AAB70741.1; --
EMBL; AF003025; AAB70741.1; --
EMBL; AF003025; AAB70742.1; --
EMBL; AF003026; AAB70743.1; --
EMBL; AF003026; AAB70743.1; --
EMBL; AF003026; AAB70743.1; --
EMBL; AF003026; AAB70743.1; --
EMBL; AF003026; AEF70743.1; --
EMBL; AF00506577
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Seedorf K., Krammer G., Durst "Human papillomavirus type 16 "Hurology 145:181-185(1985).
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Beth-Giraldo E., Giraldo G.,
Submitted (JUN-1997) to the
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PFAM; PF00527; I
Early protein; 7
DNA-binding; Tra
                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Phelps W.C., Yee C.L., Munger K.,

"The human papillomavirus type 16

transformation functions similar t
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MEDLINE; 90218027.

Schneider-Maunoury S., Pehau-Arnaudet G., Bre

"Expression of the human papillomavirus type
a line derived from a vulvar intraepithelial
J. Gen. Virol. 71:809-817(1990).
                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: HPV16, IN COMPARISON TO HPV TYPES 6 AND 1: OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN SIMILARITY: LOCAL WITH ADENOVIRUS E1A AND SV40 LT.
Trans-acting
            E7; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kalne B.P., Borodovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus annaschii.";
                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 15
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-!- SIMILARITY: WEAK, TO M.JANNASCHII MJ1342 AND TO THE
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RESULT 6
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Best Local
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15-JUL-1998
15-JUL-1998
15-JUL-1998
SEQUENCE FROM N.A.

MEDLINE; 97061201.

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Miyajima N., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okum Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaul R., Gray G.J., Koennene Kaul R., Gray G.J., Koennene ...
"Cloning and sequence analysis
"Cloning and rotein gene cluster."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of an obligate intracellular pathogen of humans Chlamydia trachomatis.";
Science 282:754-759(1998).
-i- EUNCTION: PROTEIN S5 IS IMPORTANT IN THE ASSEMBLY AND FUNCTION: THE 30S RIBOSOMAL SUBUNIT (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 99000809.
Stephens R.S., Kalman
Mitchell W.P., Olinger
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J. Bacteriol. 174:1205-1212(1992)
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Chlamydia trachomatis.
Bacteria; Chlamydiales;
                                                                                                                                                                                             Synechocystis sp.
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STRAIN=D/UW-3,
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                           TRANSMEM
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                                                                                                                        TRANSMEM
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J. Biol. Chem. 268:3099-3106(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
BACITRACIN RESISTANCE PROTEIN HOMOLOG (PUTATIVE UNDECAPRENOL KINASE)
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                                                                                                                                               Antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished observations (NOV-1994).
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Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
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    -1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
    -1 - SIMILARITY: TO E.COLI BACA.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curti B., Zanetti G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pelanda R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EC 2.7.1.66) (FRAGMENT).
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172 AA;
                                                                                                                                               resistance;
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HYPOTHETICAL PROTEIN SLR0271; 2606EEE8318D440CA CRC64;
                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of nuclear genes encoding mitochondrial proteins: isolation of a collection of D. melanogaster cDNAs homologous to sequences in the Human Gene Index database.";

MOL. Gen. Genet. 261:64-70(1999).

-1- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LINKS CF(0) TO CF(1). IT EITHER TRANSMITS CONFORMATIONAL CHANGES FROM CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.

-1- SUBUNIT: F-TYPE AIPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.

-1- SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                           EMBL; X99666; CAA67980.1; -. FLYBASE; FBgn0016691; Oscp. PROSITE; PS00389; ATPASE_DELTA; 1.
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caggese C., Ragone G., Caizzi R., Barsanti P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Etwiygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL
MITOCHONDRIAL (EC 3.6.1.34) (OSCP).
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15-FEB-2000
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                                                                                                                                                                                                                                                                  Hydrolase; ATP synthesis; CF(1); Hydrogen Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                           PFAM; PF00213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-OVARY
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[1]
                                                                                                                                                                                                                                                     CRANSIT
373 VNLLGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                      1.7%;
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01-FEB-1995
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MEDLINE; 95334362.
Burland V.D., Plunkett
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trace
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECOGENE; EG12488; yji
Hypothetical protein
SEQUENCE 212 AA; ;
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EMBL; AE000490; AAC77142.1;
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                                                                                                                                                                                                  Lamppa G.K., Morelli G., Chua N.-H.;
"Structure and developmental regulation of a wheat
major chlorophyll a,b-binding polypeptide.";
mol. Cell. Biol. 5:1370-1378(1985).
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 85295969.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Poaceae;
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mes 7; Conser
FUNCTION: THE LIGHT-HARVESTING COMPLEX (LHC) FUNCTIONS AS A LIGHT RECEPTOR, IT CAPTURES & DELIVERS EXCITATION ENERGY TO PHOTOSYSTEMS WITH WHICH IT IS CLOSELY ASSOCIATED. THE N-TERMINUS OF THE PROTEIN EXTENDS INTO THE STROMA WHERE IT IS INVOLVED WITH ADHESION OF GRANAL MEMBRANES AND PHOTOREGULATED BY REVERSIBLE PHOSPHORYLATION OF ITS THREONINE RESIDUES; BOTH ARE BELIEVED TO MEDIATE THE
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NE; EG12488;
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1. 05, Last sequence update)
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                                                                                                                                                                        "Functional analysis in yeast of cDNA coding for the mitochondrial riske iron-sulfur protein of higher plants";

Proc. Natl Acad. Sci. U.S.A. 88:10716-10720(1991).

- FUNCTION: COMPONERY OF THE UBLQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
                                                                                                                                                                                                                                                                                                              Zea mays (Maize).
Eukaryota; Viridiplantae;
euphyllophytes; Spermatoph
                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT,
PRECURSOR (EC 1.10.2.2) (RIESKE IRON-SULFUR PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlorophyll; Photosynthesis; Photosystem Thylakoid membrane; Chloroplast; Transit Transmembrane; Phosphorylation.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 92073358.
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SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE.
                                                                                   SUBUNIT: BC1 COMPLEX CONTAINS 10 SUBUNITS; 3 RESPIRATORY SUBUNITS; 2 CORE PROTEINS AND 5 LOW-MOLECULAR WELIGHT PROSUBCELLULAR LOCAFION: MITOCHONDRAL INNER MEMBRANE.
MISCELLANEOUS: THE RIESKE PROTEIN IS A HIGH POTENTIAL 2F
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                                                                                                                                     CATALYTIC ACTIVITY: QH(2) + 2 FERRICYTOCHROME 2 FERROCYTOCHROME C.
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A-B BINDIN
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peptide; Multigene family;
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R PRINTS; PRO0162; RIESAL.

R PRINTS; PR00162; RIESAL.

JR PROSITE; PS00199; RIESKE_1; 1.

DR PROSITE; PS00199; RIESKE_2; 1.

DR PFAM; PF00355; Rieske; 1.

RW Mitochondrion; Electron transport; Respiratory chain; Iron-sulfur; KW Oxidoreductase; Inner membrane; Transmembrane; Transit peptide.

MITOCHONDRION (POTENTIAL).

TRANSIT 1 61 MITOCHONDRION (POTENTIAL).

BUJIOULOUS CREDUCTASE IRON-SULFUR SULFUR SULF
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MEDLINE; 96195263.
Lindquester G.J., Inoue N.,
Stamey F.R., Dambaugh T.R.,
Frenkel N., Pellett P.E.;
                                       EMBL; L14
PROSITE;
PROSITE;
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entities
or send a
                                                                                                                                       between the Swiss Institute of Bioinformatiche European Bioinformatics Institute. These use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See )
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SEQUENCE
                   PROSITE;
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                               "Restriction endonuclease mapping and molecular cloning of therpesvirus 6 variant B strain Z29 genome.";
Arch. Virol. 141:367-379(1996).
-!- FUNCTION: PHOSPHORYLATES THE ANTIVIRAL NUCLEOSIDE ANALOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus (type Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
POSSIBLE GANCICLOVIR KINASE (EC 2.7.1.-) (FRAGMENT).
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nes 7; Conser
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SIMILARITY:
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                                                                                 L14772;
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an email to license@isb-sib.ch).
          4772; AAB06352.1;
PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_DOM;
PS50011; PROTEIN_KINASE_DOM;
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TO TYROSINE-PROTEIN
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O'Brian
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IRON-SULFUR (2FE-2S)
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BY SIMILARITY.
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Pred. No.
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an J.J., Danovich
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                                                      FALSE_NEG
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Matches 7
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Best Local
                                    LXB2_PHOLU STANDARD P23147:
01-NOV-1991 (Rel. 20, C 01-NOV-1991 (Rel. 20, L 01-NOV-1995 (Rel. 32, L ALKANAL MONOOXYGENASE BETA CHAIN).
                                                                                                            _PHOLU
Photorhabdus luminescent
Photorhabdus luminescent
Parteria; Proteobacteria;
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P40713;
01-FEB-1995
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ACT_SITE
SEQUENCE
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                             LUXB.
                                                                                                                                                                                                                                                                         EMBL; X81461; CAA57218.1; -. PROSITE; PS00583; PFKB_KINASES_1; PROSITE; PS00584; PFKB_KINASES_2;
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SEQUENCE 305
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Bacteria; P
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01-FEB-1995
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31
280 AA;
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(EC 2.7.1.
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Last annotation
BETA CHAIN (EC :
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                  (Xenorhabdus
       gamma
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Pred. No
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+ D-FRUCTOSE = ADP + D-FRUC'
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Pred. No. 27;
0; Mismatches
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Mismatches
       subdivision;
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1.14.14.3)
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                  luminescens)
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29;
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27;
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       Enterobacteriaceae
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Best Local S
Matches 7
MEDLINE; 92355513.

Medghen E.A., Szittner R.B.;

Multiple repetitive elements and organization

"Multiple terrestrial bacteria.";

Imminescent terrestrial bacteria.";

Pacteriol. 174:5371-5381(1992).
                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, C
01-FEB-1991 (Rel. 17, L
01-FEB-1996 (Rel. 33, L
ALKANAL MONOOXYGENASE B
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SEQUENCE F
STRAIN-HW;
                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 2999;
MEDLINE; 90375532.
Szittner R., Meighen E.;
Szittner R., Meighen E.;
Nucleotide sequence, expression, and prop
by lux genes from a terrestrial bacterium.
J. Biol. Chem. 265:16581-16587(1990).
                                                                                                                                                                                                                                                                                                                                                                LXB1_PHOLU P19840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and nucleotide sequences of lux genes and character of luciferase of Xenorhabdus luminescens from a human wound J. Bacteriol. 173:1399-1405(1991).

-I- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS REQUIRED FOR BIOLUMINESCENCE ACTIVITY.

-I- CATALYTIC ACTIVITY: FMNH(2) + RCHO + O(2) - FMN + RCOOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00089; LUCIFERASE.

PROSITE; PS00494; BACTERIAL_LUCIFERASE; 1.

PFAM; PF00296; bac_luciferase; 1.

Photoprotein; Luminescence; Oxidoreductase;

Flavoprotein; FMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       SEQUENCE FROM N.A. STRAIN-ATCC 29999;
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                                                                                                                                                                                                                                         Photorhabdus
                                                                                                                                                                                                                                                      Photorhabdus luminescens
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                              BETA CHAIN).
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HSSP; P07739; 1XKJ.
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57 TVSGFLL 63
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les 7; Conserv
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Last annotation update)
BETA CHAIN (EC 1.14.14.3)
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gamma subdivision; Enterc
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from a human wound.";
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Best Local S
Matches 7
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EMBL; M90093; AAA27626
EMBL; M55977; AAA27621
PIR; C37898; C37898.
HSSP; P07739; 1XKJ.
                                                                                                                                                                                                        Photoprotein; Flavoprotein; VARIANT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnston T.C., Rucker E.B., Cochrum L., Hruska K.S., Vandegrift V.;
"The nucleotide sequence of the luxA and luxB genes of Xenorhabdus luminescens HM and a comparison of the mino acid sequences of luciferases from four species of bioluminescent bacteria.";
Biochem. Blophys. Res. Commun. 170:407-415(1990).
-1- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUT REQUIRED FOR BIOLUMINESCENCE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the statement is not removed.
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Q9yeg6 aeropyrum p
Q9y2c5 homo sapien
Q61343 drosophila
Q38059 bacteriopha
Q15140 homo sapien
Q08570 catharanthu
Q19002 caenorhabdi
Q12338 human papil
Q58910 pyrococcus
G65368 unidentifie
P71192 escherichia
Q24439 drosophila
Q3wz53 thermotoga
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Q57455 caenorhabdi
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ALIGNMENTS

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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 36.9 KD PROTEIN.
HYPOTHETICAL 36.9 KD PROTEIN.
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KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L., GRIMMOOD J., DAVIS R.W., STEPHENS R.S.;

"Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";

Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AE001685; AAD19185.1; -.

SEQUENCE 333 AA; 37300 MW; 0C9213A4 CRC32;
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01-MAY-1999 (TrEMBLrel.
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ASPARTATE DEHYDROGENASE.
                                           Macaca mulatta rhadinovirus 17577.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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MEDLINE: 99174001.

X MEDLINE: 99174001.

A SEARLES R.P., BERGQUAM E.P., AXTHELM M.K., WONG S.W.;

T "Sequence and genomic analysis of a Rhesus macaque rhadi
at similarity to Kaposi's sarcoma-associated herpesvirus/hu
RT herpesvirus 8.";

RL J. Virol. 73:3040-3053(1999).

EMBL; AF083501; AAD21359.1; -.

EMBL; AF083501; AAD21359.1; -.
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                                                                                                                         01-NOV-1999 (TremBLrel. 12, ) NA/PO4 COTRANSPORTER HOMOLOG
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KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y., JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H., HOSOYAMA A., FUKUI S., NAGAI Y., NISHJIMA K., NAKAZAWA H., TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA N., SAKO Y., KIKUCHI H.;
SEQUENCE FROM N.A. MEDLINE; 99253143.
                                                                 Eutheria;
                                                                                     Eukaryota; Metazoa;
                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix K1.";
DNA RES. 6:83-101(1999).
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01-NOV-1999 (Tremblrel.
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01-AUG-1998
01-MAY-1999
                                                                                                                                                                                                                                                               MIKLOS G.L., YAMAMOTO M., BURNS R.G., MALESZKA R.; "An essential cell division gene of Drosophila, ab Saccharomyces, encodes an unusual protein with tub myosin like peptide motifs."; Proc. Natl. Acad. Sci. U.S.A. 94:5189-5194(1997).
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061343;
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                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96129280.

DE COUST H.G., FONG K.S., WEEDS A.G., MCLAUGHLIN P.J., MIKLOS G.L.;
"Molecular and mutational analysis of a gelsolin-family member encoded by the flightless I gene of Drosophila melanogaster.";
Genetics 141:1049-1059(1995).
                                                                                                                                                                                                                          MALESZKA R.,
                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=CANTONS;
                                                                                                                                                                                                                                                                                                                  STRAIN-CANTONS;
MEDLINE; 97289742.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         **SHIBUI A., TSUNODA T., SEKI N., SUZUKI Y.,

"Isolation and chromosomal mapping of a nov
homology to Na+/PO4 cotransporter.";

J. Hum. Genet. 44.190-192(1999).

EMBL; AB020527; BAA76663.1;

SEQUENCE 497 AA; 54055 MW; 128F47B4 CR
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Best Local S
Matches 7
   SEQUENCE FROM N.A. STRAIN=(L.) G.DON; MEDLINE; 93283641. MEIJER A.H., SOUER I
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Q08570;
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ
EMBL; AF005898; AAB61675.1; -
PFAM; PF00287; Na_K-ATPase; 1.
SEQUENCE 63 AA; 7591 MW; 4F685A8E CRC32;
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
NA,K-ATPASE BETA-3 SUBUNIT PSEUDOGENE, COMPLETE SEQUENCE.
                                                                                                                                                                                                            Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophyta; permatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae;
                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME P-450 (EC 1.14.14.1) (CR9) (FRAGMENT).
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MALIK N., CANFIELD V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; C
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Viruses; dsDNA viruses,
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EMBL; M11813; AAA88482.1;
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   VERPOORTE
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Best Local S
Matches 7
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MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

MILSON R., AINSCOUGH R., CONNELL M., COPSEY T., COOPER J., COULSON A.,

A BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

A CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

A GARDNER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.,

A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAATREILLE P.,

A JONES M., KERSHAW J., KIRSTEN J., MORTIMORE B., O'CALLAGHAN M.,

A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

A PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

A PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

A PARSONS J., THOMAS K., VAUDIN M., VAUGHLM K., WATERSTON R.,

A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

T "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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019002;
01-NOV-1996 (TIEMBLIEL COL-NOV-1996 (TIEMBLIEL COL-NOV-1998 (TIEMBLIEL COL-NOV-1998 (TIEMBLIEL COL-NOV-1998)
                                                                                                                                                        WATERSTON R.;
Submitted (NOV
EMBL; U40800;
SEQUENCE 97
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SEQUENCE
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Eukaryota; Metazoa; Ner
Rhabditina; Rhabditoide
                                                                                                                                                                                                                                                                                                                                                             Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                   GEISEL
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    305 LSCGLST
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                                           7; Conserv
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(NOV-1995) to the EMBL/GenBank/DDBJ
1800; AAA81489.1; -.
97 AA; 11281 MW; E5A676F5 CRC32;
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ilarity 100.0%
Conservative
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                Score 7; Pred. No.
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                                                Mismatches
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012338;
01-JUL-1997
01-JUL-1997
01-NOV-1998
276 ILGSLPS 282
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116 ILGSLPS 122
                                                                                                                                                                                                                                                                                                                          "Complete sequence and gene organization thermophilic archaebacterium, Pyrococcus DNA Res. 5:55-76[1998].
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KAWARRBAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
KAWARRBAYASI Y., SAWADA M., HORIKAWA H., HOSOYAMA A., NAGAI Y.,
YAMANOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OGUCHI
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA
KIKUCHI H.;
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01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
128AA LONG HYPOTHETICAL
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J. Gen. Virol. 78:0-0(0).
EMBL; AF003022; AAB70739.1; -
PFAM; PF00527; E7; 1.
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TORNESELLO M.L., BUONAGURO F.M., MEGLIO BETH-GIRALDO E., GIRALDO G.;

"Sequence variations and viral genomic s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus horikoshii.
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                                                                                                                     Local Similarity
nes 7; Conserv
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RNA
                                                                                                              Score 7; DB 1; Pred. No. 38; 0; Mismatches
                                                                                                                     0;
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P71192;
01-FEB-1997
01-FEB-1997
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                   SMITH C.A., THOMAS C.M.;
"Comparison of the nucleotide sequences of the vegetative replication origins of broad host range IncP plasmids R751 and RK2 reveals conserved features of probable functional importance.";
Nucleic Acids Res. 13:557-572(1985).
EMBL; U67194; AAC64458.1; -.
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01-AUG-1998;
01-AUG-1998;
01-NOV-1999
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Plasmid IncP-beta R751.
Bacteria, Proteobacteria,
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OHKUMA M., NODA S., KUDO T.;
Submitted (MAR-1998) to the
EMBL; AB011958; BAA28491.1;
HSSP; P00456; 1CP2.
                                                                                                                       136 VYYIPTY
                                                                                                                                                             217 VVYIPTY
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PS00746; NIFH_FRXC_1;
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RESULT O9W253 JD W253 JC W252 
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MOI. Gen. Genet. 261:64-70(1999).

CF(0) TO CF(1). IT EITHER TRANSMITS COMPORMATIONAL CHANGES FROM C CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.

C CF(0) INTO CF(1) OR IS IMPLICATED IN PROTON CONDUCTION.

C CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE C CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE C SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)

C HAS THREE MAIN SUBUNITS: A, B AND C.

C -: SIMILARITY: BELONGS TO THE ATPASE DELTA CHAIN FAMILY.

DR EMBL; X99666; CAA67980.1; -.

DR PROSITE: PS003189; ATPASE_DELTA; 1.

DR PROSITE: PS00313; OSCP; 1.

DR PFAM; PF00213; OSCP; 1.

THE ATPASE DELTA.

THE ATPASE DELTA.
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Matches 7
NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
HART D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HBIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
SMITH H.O., VENTER J.C., FRASER C.M.;
"Evidence for lateral gene transfer between Archaea and bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U1-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9WZ53
O9WZ53;
O1-NOV-1999 (TIEMBLTel. 12,
O1-NOV-1999 (TIEMBLTel. 12,
O1-NOV-1999 (TIEMBLTEL. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of nuclear genes encoding mitochondrial proteins: isolation of a collection of D. melanogaster cDNAs homologous to sequences in the Human Gene Index database.";
Mol. Gen. Genet. 261:64-70(1999).
-I- FUNCTION: THIS PROTEIN SEEMS TO BE PART OF THE STALK THAT LIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrembLrel. 01, Created)
01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-NOV-1996 (TrembLrel. 12, Last annotation update)
ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR,
MITOCHONDRIAL (EC 3.6.1.34) (OSCP).
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 99287316.
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Mitochondrion; Transit peptide.
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TISSUE-OVARY;
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Search completed: May Job time: 399 sec
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                                                                                                                            Query Match
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Matches 7
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SEQUENCE FROM N.A.
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NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
NAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.J.
SMITH H.O., VENTER J.C., FRASER C.M.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AE001733; AAD35669 1; -.
EMBL, AE01733; AAD35669 1; -.
                                                                                              110 LSGMLLG 116
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Search time (sec): 602.2600
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-Q-/cgn2_1/USP70_spco1/US99391958/runat_24052000_213605_8816/app_query.fasta.1
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-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-60.000 -YGAPEXT-60.000
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-TRANS-human41.cd1 -LIST-45 -DOCALIGN-200 -THR_SCORE-quality
-THR_MIN-1 -ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US09391958 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
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609
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                                                                                                                                                                                      BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
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TITLE
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AA858296 609 bp mRNA EST 09-MAR-1998 obl3b06.sl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323539 3' similar to TR:000476 000476 SODIUM PHOSPHATE TRANSPORTER. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
On Jan 19, 1998 this sequence version Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 609)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Cancer Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop:
Location/Qualifiers
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/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
/lab_host="DH10B"
/note="Organ: kidney: Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert_Strausberg@nih.gov
M. Fatima Bonaldo.
1 118 c 114 g
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Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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| C68800 C68800 Yuji Kohara un
| AQ191156 HS_2195_B2_A05_MR C
| AA104994 m180c05.rl Stratage
| AI587324 tq04h05.xl NCI_CCAP
| AW326686 19580 MARC 2BOV Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project (CGAP),
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Gaps: Percent Identity:

Length:

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              BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nValLeuAspIleAlaProArgTyrSerSerPheLeuMetGlyAlaSerA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:803109
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 243)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor
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Location/Qualifiers
            75
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(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. " 57 c 50 g 61 t
                                                                                                                                         /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer; double-stranded cDNA was ligated to Eco RI adaptors
                                                                                                                                                                                                                                                              /clone="IMAGE:1761689"
/clone_lib="NCI_CGAP_Kid3"
                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                                                                                               /lab_host="DH10B"
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REFERENCE
AUTHORS
TITLE
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LOCUS AI792430
                                                                                                                                                                                                                                                                                                                                          SOURCE
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US-09-391-958-1 x AI222455/rev
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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAACTCACTCGTTTA 28
                                                                                                                                                                                                                                                                                                                                                                                            AIT92430 244 bp mRNA EST 02-JUL-1999 gg21b09.y5 NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1761689 similar to SW:NPT4_HUMAN 000476 SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 4 ;, mRNA sequence.
          CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                    On Jun 5, 1998 this sequence version replaced gi:3187571 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                    Unpublished (1997
                                                                                                                                                                                                                            NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Dental Research,
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Eutheria; Primates;
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                                                                                                                                        Email:
                                                                                                                                                                                                                Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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                                                                                                                                                                                                                                                                       (bases 1 to 244)
                                                                                                                               Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
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                              information can be
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new read against
Putative full length read
The vector to vector length is

This 5' resequenced clone

has

no

previous

ú

data

to verify this

245

This read is a RESEQUENCE of a previously sequenced human Original clone citation: see original entry for original cinformation

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SOURCE
ORGANISM
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LOCUS AT244777
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ORIGIN
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                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGly 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAAGAGGATTTTCGAGCATAGCACCTGTCATTGTACCCACTGTCAGCGG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est24:AI244777
                                                                                                                                                                                                                                                                                                                                                                                                   AI244777 297 bp mRNA EST qj92f01.x1 NCI_CGAP_Kid3 Homo sapiens cDNA clone similar to SW:NPT4_HUMAN 000476 SODIUM-DEPENDENT TRANSPORT PROTEIN 4 ;, mRNA sequence.
                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                      On Jan 19, 1998 this sequence version replaced gi:2045043 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                    Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 297)
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cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D.
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/db_xref="taxon:9606"
/clone="ITMAGE:1761689"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
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= IMAGE:1866937
| PHOSPHATE
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US-09-391-958-1 x AI244777/rev
                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AI733707
                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est32:AI733707
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                                           TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
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                                                                                                                                                                                                                                                                                                                                                                                                                               63
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Ratio:
                                                                                                                                                                                                                                               AI733707 211 bp mrNA EST qg21b09.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone similar to SW:NPT4_HUMAN 000476 SODIUM-DEPENDENT TRANSPORT PROTEIN 4 ; mRNA sequence.
Cancer Genome Anatomy Project 
Unpublished (1997)
                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 211)

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research.
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                              AI733707.1 GI:5054820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"; Vector: pT7T3D-Pac (Pharmacia) with note="organ: kidney; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "Te
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/db_xref="taxon:9606"
/clone="IMAGE:1866937"
/clone_lib="NCI_CGAP_Kid3"
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JOURNAL

Michael

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Research,

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BASE COUNT
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LOCUS AIB21963
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ACCESSION
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                                                                                                                                                                                                                                                             391 GluTrpAlaLysGluArgLysLeuThrArgLeu 401
                                                                                                                                                                                                                                                                                                                                                                    374 snLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyGluAlaAspValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 nAspProGluPheGlyTrpArgAsnValPhePheLeuLeuPheAlaValA 374
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          AI821963 452 bp mRNA EST obl3b06.x5 NCI_CGAP_Kid3 Homo sapiens cDNA clone similar to SW:NPT4_HUMAN 000476 SODIUM-DEPENDENT TRANSPORT PROTEIN 4 ; mRNA sequence.
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This read has been verified (found to hit its original self in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correct orientation)
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Gaps: 0
Percent Identity: 100.000
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IMAGE:1323539
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Percent Similarity: 100.000
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                                   388 spValGlnGluTrpAlaLysGluArgLysLeuThrArgLeu 401
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                                                                                                                                                                   371 eAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyGluAlaA 388
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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On Mar 10, 1998 this sequence version replaced gi:2948996
Other_ESTs: ob13b06.y5
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National Cancer Institute / National Institute of Dental
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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EST.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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M. Fatima Bonaldo. "
84 c 78 g 175 t
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/clone_lib="NCI_CGAP_Kid3"
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US-09-391-958-1 x AA706766/rev
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                                                                                                                                                                                                                                  Quality: 44.00
Ratio: 1.000
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                                                                                      339 PheSerSerIleAlaProValIleValProThrValSerGlyPheLeule 355
355 uSerGlnAspProGluPheGlyTrpArgAsnValPhePheLeuLeuPheA 372
                                           216 TTTTCGAGCATAGCACCTGTCATTGTACCCACTGTCAGCGGATTTCTTCT 167
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost Hillier,L., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 5, 1995 this Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSPORTER. ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                     103
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                                                                                                                                                                                                                                                                                                                                                                                                                                  constructed by Bento Soares and M.Fatima Bonaldo."
73 c 65 g 80 t
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/db_xref="GDB:1331118"
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                                                                                                                                                                                                                                           Percent Identity: 100.000
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Gaps:
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REFERENCE
AUTHORS
TITLE
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                                       alignment_block:
US-09-391-958-1 x AI247271/rev
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Align seg 1/1 to reverse of: AI247271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2286652.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST.
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1 (bases 1 to 173)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                        52
                                                                                                           : 1.000
: 100.000
                                                                                                                                                                                                                                                               /note-*Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1863885"
/clone_lib="NCI_CGAP_Kid3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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385 GlyGluAlaAspValGlnGluTrpAlaLysGluArgLysLeuThrArg 400

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seq_documentation_block:
LOCUS AI196449
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ORIGIN
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Percent Similarity: 100.000
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JOURNAL
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                                                                                                                                                                                                                                                                                                   AII96449 454 bp mRNA EST ui69h08 x1 Sugano mouse liver mlia Mus musculus IMAGE:1887711 3', mRNA sequence.
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
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Other GSSs: RPCIII-11K11.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
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1 (bases 1 to 495)
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RPCI11-11K11.TP RPCI-11
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/db_xref="GDB:7504090"
/db_xref="taxon:9606"
/clone="RPCI-11-11K11"
/clone_11b="RPCI-11"
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="TecoRI" | Site_2: EcoRI; Site_2: EcoRI;
/note="Nature: PACE: PA
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LOCUS AV267452 270 bp mrNA EST 05-NOV-1999 DEFINITION AV267452 RIKEN full-length enriched, adult male testis (DH10B)
                              seq_documentation_block:
LOCUS AV267452
                                                                                                       seq_name: gb_est41:AV267452
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US-09-391-958-1 x AI196449
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                                                                                                                                                                                                    275 ThrileLeuGlySerLeuProSerSerAla 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                    89 ACGATCCTGGGTAGCCTTCCTTCCAGTGCT
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Ratio:
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AI196449.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: custom primer used High quality sequence stop: 44:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse
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: 1.000
: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pMELBS-FL3 vector [5' site CACTGTGTG, 3' site CACCATGTG). XhoI show the used to isolate the cDNA insert. Size selection was performed to exclude fragments 41.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAAGCTGCG and 3' en primer CGACCTGCACCTCGACCACA."

120 c 107 g 127 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1887711"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="adult"
/lab_host="DH10B"
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On May 14, 1999 this sequence version replaced g1:4827795. Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute of Physical and Chemical Research
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-res@rtc.riken.go.jp,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      visit our web site (http://genome.rtc_riken.go.jp) for
/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken
                                                                                                       prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="4930526G11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, adult male testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
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                              CDNA
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alignment_block:
US-09-391-958-1 x AV267452/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Feb 17, 1998 this sequence version replaced g1:2889559. Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R. Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Barter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Possible reversed clone: similarity on wrong strand High quality sequence stop: 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone was previously sequenced on data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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                             /lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: xhol; Cloned unidirectionally. Primer:
Oligo dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GARTTTTTTTTTTTTTTTTT 3'"
     sequence:
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6"
                                                                                                                                                                                                                                   /dev_stage="ll weeks old"
                                                                                                                                                                                                                                                                                               /sex="females"
                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:522551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                              'tissue_type-"whole skin"
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the 5' end only, this n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          end only, this
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US-09-391-958-1 x AI427938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1292357.
Contact: Masria MyMouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 314 200 100 Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This_clone is available royalty-free through LLNL; contact the
This_clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vc3la07.rl Barstead MPLRB1 Mus musculus cDNA clone IMAGE:776148 5/similar to TR:G887523 G887523 SODIUM-PHOSPHATE TRANSPORT SYSTEM 1., mRNA sequence.

AA276173
                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 459.
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Eukaryota; M
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EST.
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                124
      /tissue_type="Kidney"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
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                                                                                                                                                                                                                                                    /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                    /clone_lib="Barstead MPLRB1"
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3867
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (Info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 942 row: L column: 21
Seq primer: SP6
Class: BAC ends
                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Feb 19, 1999 this sequence version replaced gi:4129789
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A0570823 499 bp DNA GSS 01-JUN-1999 HS 5366_B1_F11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=942 Col=21 Row=L, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 499)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hood, L
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
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                            Ratio:
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  : 9.00
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                                                                                                                                                           /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 71 c 100 g 174 t 5 others
                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=942 Col=21 Row=L"
                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                               /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                    location/Qualifiers
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US-09-391-958-1 x AW067082
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                                                                              Align seg 1/1 to: AW067082
                                                                                                                                                                         Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
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Ea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

E 1 (bases 1 to 523)

Walbott V.

Malze ESTs from various cDNA libraries sequenced at Stanford University
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:ll35638.

Contact: Walbott V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                               Quality:
Ratio:
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AW067082 AW067082.1 GI:6022154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: walbotéstanford.edu
Plate: 683015 row: C column: 02.
Cocation/Qualifiers
1. .523
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                                                                                                                                                                                                                                                                                                                   D
                                                                                                                                                                                                                                                                                                             /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap
Express); Site_1: XhoI; Site_2: EcoRI; Directionally
cloned, 14 day immature embryo library created with
Stratagene's Zap Express cDNA protocoi."
a 160 c 177 g 94 t
                                                                                                                                                                                                                                                                                                                                                                                                                    /tlssue_type="embryo"
/dev_stage="14 days after pollination"
/lab_host="DH10B"
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/cultivar-"B73"
/db_xref-"taxon:4577"
/clone_lib="683 - 14 day immature embryo from Hake lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SH)
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Percent Identity: 100.000
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Protein involved i
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Query Match 100.0%; Best Local Similarity 100.0%; Matches 401; Conservative 0;

Score 2076; DB 1; Pred. No. 3.3e-213;); Mismatches 0;

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1 MQVDETLIPRKVPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDS 60

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New isolated human sodium-dependent phosphate to develop products for treating e.g. cancers, Alzheimer's disease, diabetes, encephalopathy, hypocalciuria or hypoglycaemia. Claim 1; Fig 1; 66pp; English. This sequence is the human sodium-dependent ph (NAPTR) of the invention. NAPTR and agonists of prevent disorders associated with decreased e.g. cancers of the kidney, disorders of decre including tumoural calcinosis, osteomalacia, o hypophosphatemia, rickets, cysteneuria, nephroposphatemia, rackets, cysteneuria, nephroposphatemia, rickets, cysteneuria, nephroposphatemia, rickets, cysteneuria, nephroposphate, racidomyopathy, mypokalaemia, external ophthalmoplegia, Kearns-Sayre syndrom encephalopathy, cardiomyopathy, hypokalaemia, disorders of cell signalling through cAMP, ATP glucose-6 phosphate levels, e.g. hypocalciuria abnormal phosphate regulation in neurons, gast liver. The products can also be used for detec screening. Sequence 401 AA;	1 9971 standard; 9971; 9971; 9971; 9971; 9971 (fix nan sodium-dependent 11 signalling of mo sapiens. 9837198 -A1FEB-1998; UO37 -FEB-1997; US-8 -FEB-1998;	103.5 5.0 488 103.5 5.0 514 103.5 5.0 561 103.5 5.0 2723 103.5 5.0 606 102.5 4.9 559 102.5 4.9 2841 101.5 4.9 537 99.5 4.8 2969 99 4.8 456
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(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RoRet gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can similarly be used for hypophosphatemia. The present sequence represents
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Best Local Similarity
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feder JN, Kronmal GS, La Tsuchihashi Z, Wolff RK; WPI; 98-240014/21.
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07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
(PROG-) PROGENTIOR INC.
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Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 60; Fig
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30-SEP-1997; U17658.
07-MAY-1997; US-552495.
01-OCT-1996; US-724394.
(PROG-) PROGENTIOR INC.
Feder JN, Kronmal GS, Laue
Tsuchihashi Z, Wolff RK;
                  DNA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RORet gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can similarly be used for hypophosphatemia. The present sequence represents
                 NTP3.
                                                                                                                                                                                                                                                       products from the human haemochromatosis gene. Also described is a method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                         Claim 54; Fig 5B; 209pp; English.
The present invention describes hereditary haemochromatosis
Sequence
                                                                                                                                                                                                                        haemochromatosis (HFE) gene mutation in an individual comprising:
(a) providing DNA or RNA from the individual; and (b) assessing the
                                                                                                                                                                                                                                                                                                                                metabolism
                                                                                                                                                                                                                                                                                                                                              Hereditary haemochromatosis gene
for the diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09814466-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human haemochromatosis protein NTP3.

Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF2; BTF3; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V57909.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Matches 112
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N-N-PSDB; 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1997 (first entry)
Human brain sodium-dependent inorganic phosphate cotransporter.
Brain sodium-dependent inorganic phosphate cotransporter; hBNPJ
                                                                                                                                                                                                                   human hippocampus cDNA library. hBNPI can be expressed in transformed host cells and used to determine the effectiveness of test cpds. for the treatment or prevention of disorders associated with an inappropriate stimulation of hBNPI.
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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27-APR-1995;
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                                                                                      Local Similarity 28.
nes 112; Conservative
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                                          12 VPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDSSEVLPVDSFGG
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96-497773/49.
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                                                                                      62;
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Query Match
Best Local S
Matches 112
                                                                                                                                                                                                         countertransporter (ISCT) BNPI. A DNA sequence for human BNPI is provided (see V33503). LSCTs such as BNPI provide the physiological mechanism for the extrusion of lithium from cells, i.e. it regulates the cell concentration of lithium. Its activity determines the therapeutic effect of lithium. The invention provides a simple molecular biological test for the ability of cells to extrude lithium. The LSCTs have significance for cells to extrude lithium. The LSCTs have significance for determining the responsiveness of humans with mental disorders, including manic depressives, to treatment with lithium salts. Probes and primers for BNPI, PIT-1 (see W70499) can be used in diagnostic tests useful for genetic screenings to predict whether a patient will respond to lithium calls that the test is also a screen for susceptibility to, and extent of, manic depressive illness, and is suitable for screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated lithium-sodium counter-transporter DNA - used to develop products for evaluating lithium-sodium transport in erythrocytes, particularly for lithium therapy in manic depression claim 8; Page 45-47; 64pp; English.

This polypeptide comprises the brain-specific human lithium-sodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gunn RB, Timmer RT WPI; 98-520759/44. N-PSDB; V33503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JAN-1999 (first entry)
Human sodium-lithium countertransporter BNPI.
Sodium-lithium countertransporter; sodium-phosp
BNPI; human; lithium therapy; manic depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W70500
                                                                                                                                                           Sequence
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WO9838203-A1.
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27-FEB-1997;
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                                 Similarity
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US-039462.
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Score 479; DE
Pred. No. 1.26
68; Mismatches
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DB 1;
1.2e-42;
nes 155;
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                                                              Length
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                                                                                                                                              PT Identifying agents for treating or preventing neurodegeneration - PT Identifying agents for treating Allheimer's disease useful for, e.g. potentially treating Allheimer's disease PT useful for, e.g. potentially treating Allheimer's disease PT useful for, e.g. potentially treating Allheimer's disease PT processoure; Fig 3; 66pp; English.

CC elegans: The eat-4 gene is a cAMP regulatory gene. The specification CC describes the identification of compounds for treating (or preventing CC areporter gene linked to a cAMP (cyclic adenosine monophosphate) CC are gulatory gene or promoter, with a test compound and measuring CC expression of the reporter gene. Such compounds are potentially useful for treating and preventing Alzheimer's, Parkinson's and Huntington's CC diseases, amyotrophic lateral sclerosis, multiple sclerosis, stroke or CC diseases, amyotrophic lateral sclerosis, multiple sclerosis, stroke or CC canoriabditis elegans, constitutive activation of the GTP-binding CC some genes, including adenylyl cyclase-type genes, block Gas-induced cell death, suggesting that the effect of Gas is associated with changes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                                           Matches
                                                                       Query Match
Best Local
                                                                                                                          death, sugyester
cAMP levels.
                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-1997; US-864785.
(GEHO ) GEN HOSPITAL CORP.
Hart AC, Kaplan JM, Oppenl
WPI; 99-045345/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-MAR-1999 (first entry)
Eat-4 protein amino acid sequence.
Eat-4 protein; cAMP regulatory gene; neurodegeneration; cAMP;
Cyclic adenosine monophosphate; reporter gene; Alzheimer's; Parkinson's;
Huntington's disease; amyotrophic lateral sclerosis; multiple sclerosis;
stroke; epilepsy; GTP-binding protein G alpha s; Gas;
adenylyl cyclase gene; Gas-induced cell death; cAMP level.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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                                                          Local Similarity nes 101; Conserv
                             92 IWERWGPPQERSRLCSIALSGMLLGCFTAILIGGFISETLGWPFVFYIFGGVGCVCCLLW 151
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  JM, Oppenheimer
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                                                                       22.5%;
32.3%;
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                                                       Score 466.5; DB 1;
Pred. No. 2.7e-41;
5; Mismatches 134;
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14-JAN-1997.
03-JUL-1995;
03-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein involved in cephalosporin C biosynthesis. cephalosporin C; biosynthesis; fermentation. Acremonium chrysogenum. 109009966-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 9-11; 21pp; Japanese.
This protein, encoded by DNA derived from Acremonium chrysogenum, involved in biosynthesis of cephalosporin C. The gene involved in biosynthesis of cephalosporin C or its cDNA can be used to improve fermentation ability of Acremonium chrysogenum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chrysogenum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acremonium chrysogenum cephalosporin C - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W14439 standard; Protein;
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WPI; 97-126424/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY-1997
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LLSQDPEFGWRNVFFLLFAVNLLGLLFYLI-FGEA
                                                                                                                                                                                                                                                                                                                                                ERGRAMAIWTEGPLMGPAVGPAVGGYLAEAKGWRWVFWVVAIGGGFITGMFFLIARE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                           QERSRLCSIALSGMLLGCFTAILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIYDDP 159
                                                                                                                                    GQASDRILSKKSGGMELKPEFRLPLM-----IP-GAFCIPMCFFIYGWATYYKLHW
                                                                                                                                                                               GYLADFILTKK-----FRLITVRKIATILGSLPSSALIVSLPYLNSGYIT-----
                                                                                                                                                                                                                                                                         I---WSICLG-CFSHQWLVSTMVVYIPTYISSVYHVNIRDNGLLSALPFIVAWVIG-MVG
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                                          MMPICATSLLGIGLNLSLMT---IQVYLVDTYTLYSASALAAATILRSLFGAFLP-LAGP
                                                                                                                                                                                                                                                                                                                      -TYPPVLLQRK----VNRLRQETGN---PLLTSALADTSSRRARISRSVRRPLVLLFRS-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSTTAVRKIFNCGGFGGEAAFMLIVAYTTSD-TTAIMALIAAVGMSGFAISGFNVNHLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FVVIYDDPVSYPWISTSEKEYIISSLKQQVG--SSKQP----LPIKAMLRSLPIWSICLG
                                                                                                                                                                                                                               IVFLFSVFIAVVFSYQFL---LFVTIPSVFGEIYDFSLGQIG-LSYLGIAAGLLLGNAIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEADVQEWAKERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APRYAAILMGFSNGIGTLAGLTCPFVTEAFTAHS-KHGWTSVFLLASLIHFTGVTFYAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RLIT-VRKIATILGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFARSWTFYLLLQNQLTYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLADYLRSNKI
                                                                                       ----ATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP-167461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene involved in biosynthesis to improve fermentation abilit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 169.5; DB 1;
Pred. No. 9.9e-10;
62; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fermentation ability of A.
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                                          436
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В

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PLYDALGLGWGNSTLGFIAVALIPVPFLFIRYGEA

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                                                                                                                                                            Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells and a process for producing the TR protein are claimed. TR polypeptides and polynucleotides are useful for diagnosing diseases related to over or under expression of TR protein by identifying mutations in the TR gene, or determining TR polypeptide or mRNA expression levels due to an infection of an organism with the TR gene (claimed). They can diagnose the stage and type of infection TR is also useful for screening for compounds which affect the TR activity. These can be used in treatment to inhibit (antagonist i.e. antibacterial drugs) or enhance (agonist) TR activity. Direct administration of TR polypeptides can be used to treat conditions associated with a lack of TR (claimed). Direct administration of
                                                                                                                                                                                                                                                                            respiratory tract (e.g. otitis media), cardiac (e.g. infective endocarditis), gastrointestine (e.g. splenic abscess), CNS (e.g. cerebral abscess), eye (e.g. conjunctivitis), kidney and urinary tract (e.g. epididymitis and toxic shock syndrome), skin (e.g. wound infection), and bone and joint (e.g. septic arthritis). TR polypeptides, polynucleotides and their (ant)agonists can prevent adhesion of bacteria to matrix proteins, and are useful for use on wounds and body implants to prevent bacterial infection. TR is
                                                                                                                                                                                                                                                                                                                                                                                                                                                           antisense oligonucleotides prevents expression. TR polypeptides (administered directly, in a vector (gene therapy) and as a vaccine) and antibodies induce an immune response to immunise and prevent disease (claimed). Diseases diagnosed, prevented or treated include: bacterial, especially S. aureus, infections of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid of a novel tetracycline resistance protein (TR) of Staphylococcus aureus WCUH29 (NCIMB 40771) thta is involve in sugar or drug transport across bacterial cytoplasmic membranes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Staphylococcus aureus tetracycline resistant protein and gene useful as diagnostic reagents and for prevention and treatment of staphylococcal infections, including toxic shock syndrome and otitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TR polynucleotide (see X07357) has been isolated from an S. aureus DNA library. Vectors comprising the claimed polynucleotide, host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 27-29; 35pp; This is the amino acid of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; X07357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burnham MKR, Lonetto MA, Warren PV; WPI; 99-097783/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epididymitis; toxic shock syndrome; sepsis; septic arthritis;
diagnosis; therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetracycline resistance; antibiotic; antibacterial; screening; infection; otitis media; endocarditis; abscess; conjunctivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W97820 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUL-1998; 305495.
23-JUL-1997; US-898976.
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                                                                                                                                                     Local 5.
  130
                                                                                92
                                        77
                                                                                                                    20
                                                                                                                    YGIALVLHFCNFTTIAQNVIMN---ITMVAMVNSTSPQSQLNDSSEVLPVDSFGGLSKAP 76
                                     KSLPAKSSILGGQFAIW-ERWGPPQERSRLCSIALSGMLLGCFTAILIGGFISETLGW--
                                                                              YGVILII----FGSIIGNIFQHQSPLTLVGRIIQTA--
                                                                                                                                                                                 Similarity
                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aureus tetracycline resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 462
-LYVIYVAKYLSKEDQKTYLGLSTSSYSLSLVIGTLSGGFIFTYLHWTN
                                                                                                                                                                               5.9%;
17.7%;
                                                                                                                                                          86;
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                                                                                                                                                                             Score
Pred.
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                                                                                                                                                              Mismatches
                                                                                                                                                                               122.5;
No. 9.
                                                                                                                                                                                 .6e-05;
                                                                                                                                                                                                  DB 1;
                                                                                                                                                            158;
                                                                                                                                                                                                Length
                                                                                                                                                            Indels
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                                                                                                                                                                                                    462;
                                                                                                                                                            109;
                                                                              -GLAAAE
                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                            Gaps
                                   134
                                                                              129
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132 637 Qy

79

LPFVSMILGLANLVLYFRWMGPQ---

LPAKSSILG-GQFAIWERWGPPQERSRLCSIALSGMLLGCFTAILIGGFISET-----L

-RLMFLVLWKLARGAFPLALLMG-ISATEGRTSVL 692

Query Match
Best Local Similarity
Matches 97; Conser

Conservative

35;

Mismatches

Indels 123; Length

Gaps

23;

5.48;

Score 112.5; Pred. No. 0.

; DB 133;

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2969;

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693

GAEFCFDVTFEVDTSVLGWV-VASVVAWAIALLSSMSAGGWRHKAVIYRTWCKGY--QAL GWPFVF-----YIFGGVGCVCCLLWFVVIYDDPVSYPW-----ISTSEKEYIISSL 177

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                                                                                                                                                                                                       28-APR-1998.
10-AUG-1997;
10-AUG-1996;
                        diseases caused by virus claim 1; Pages 108-112; 128pp; Japanese.

The present sequence represents a fragment of a new Hepatitis g virus protein (see also W56441-50 for other fragments). RNA was synthesised from the serum of nine patients judged positive for Hepatitis g virus and cDNA synthesised from this RNA. The cDNA was used as a template in several PCR reactions to isolate fragments of the new gene. The gene may be useful for diagnosing and developing treatments for Hepatitis g
                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1998 (first entry) Fragment HGJ2141 of a new Hepatitis virus g
                                                                                                                                           New hepatitis G virus gene - useful for
                                                                                                                                                                                                                                                                                                Misc_difference 1448.
                                                                                                                                                                                                                                                                                                                                           Misc_difference 1388.
                                                                                                                                                                                                                                                                                                                                                                   Hepatitis g virus gene; diagnosis;
Hepatitis g virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            W56446
               virus diseases
                                                                                                                                                               N-PSDB; V23080
                                                                                                                                                                             WPI; 98-304974/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAVGNHISIFVISMIFFAGSFALMYAPL-LNEAIKT-----IDLNMTGVAIGFYNLIINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---YMIGALIAIIVFALYIKNAQRPLVNKSFFQNKRYASFLFIVFVMYAIQLGYIFTFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQEWAKERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRGFSSIAPVIVPTVSGFLLSQDP-----EFGWRNVFFLLFAVNLLGLLFYLIFGEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMEQIYHLQLDTTSLLLVPGYIVAVIVGALSGKIGEYLNSKQAIITAIILIALSL-ILPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKEYIISSL-----KQQVGSSKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 2969 AA.
                                                                                                                                                                                          BML KK.
    2969 AA;
                                                                                                                                                                                                          227387.
JP-227639.
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                                                                                                                                                                                                                                                                                                .1467
                                                                                                                                                                                                                                                                                                            "nucleotides of given in the
                                                                                                                                                                                                                                                                "nucleotides encoding these residues given in the specfication"
                                                                                                                                                                                                                                                                                                           given
                                                                                                                                                                                                                                                                                                                                                                                    treatment; Hepatitis
                                                                                                                                                                                                                                                                                                           encoding these specfication"
                                                                                                                                             diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                           residues
                                                                                                                                              treating
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W5645D

W5045D

W5045D

W505D

W505D
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Best Local Similarity
Matches 91; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New hepatitis G virus gene - useful for diagnosing and treating diseases caused by virus claim 1; Pages 133-127; 128pp; Japanese.

The present sequence represents a fragment of a new Hepatitis g virus protein (see also W56441-50 for other fragments). RNA was synthesised from the serum of nine patients judged positive for Hepatitis g virus and cDNA synthesised from this RNA. The cDNA was used as a template in several PCR reactions to isolate fragments of the new gene. The gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reayment F1029 of a new Hepatitis virus g protein.
Hepatitis g virus gene; diagnosis; treatment; Hepatitis g virus
Hepatitis g virus.
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N-PSDB; V20384.
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WPI; 98-304974/27.
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Fragment HGJ1916 of a new Hepatitis virus g protein.
Hepatitis g virus gene; diagnosis; treatment; Hepati
Hepatitis g virus.
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10-AUG-1996;
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MGLPV----VARRGDEVLIGVLQDVNHLPPGFVPTAPVVIRMCGQGSLGVTRAALTGRDP
                                           SGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPT---
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8; Mismatches 133;
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RESULT
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RESULT
W56443
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Best Local S
Matches 91
W56443 standard; Prot
W56443;
31-JUL-1998 (first e
Fragment HGJ1741 of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New hepatitis G virus gene - useful for diagnosing and treating diseases caused by virus (diseases caused by virus (claim 1; Pages 89-93; 128pp; Japanese. The present sequence represents a fragment of a new Hepatitis g virus protein (see also W56441-50 for other fragments). RNA was synthesised from the serum of nine patients judged positive for Hepatitis g virus and cDNA synthesised from this RNA. The cDNA was used as a template in several PCR reactions to isolate fragments of the new gene. The gene may be useful for diagnosing and developing treatments for Hepatitis control of the server of the new gene.
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Sequence 2873 AA;
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Fragment HGJ606 of a new Hepatitis
Hepatitis g virus gene; diagnosis;
Hepatitis g virus.
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10-AUG-1996; JP-227639.
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                                                                          Protein;
a new
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Hepatitis
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treatment; Hepat
  Virus
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protein.
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10-AUG-1997;
10-AUG-1996;
(BMLB-) BML KI
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Hepatitis
             The present sequence represents a fragment of a new Hepatitis g virus protein (see also W56441-50 for other fragments). RNA was synthesised from the serum of nine patients global positive for Hepatitis g virus and cDNA synthesised from this RNA. The CDNA was used as a template is several PCR reactions to isolate fragments of the new gene. The gene may be useful for diagnosing and developing treatments for Hepatitis
                                                            New hepatitis G virus gene - diseases caused by virus Claim 1; Pages 97-101; 128pp;
                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Sequence
        virus diseases
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JP-227639.
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                                                                             treating
                                   titis g virus
synthesised
itis g virus
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750
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                                  KQQV----
                                                                                                                                      LPFVSMILGLANLVLYFRWMGPQ---RLMFLVLWKLARGAFPLALLMG-ISATRGRTSVL
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RQRVVRSPLGEGRPTKPLTI--
                                                                 GAEFCFDVTFEVDTSVLGWV-VASVVAWAIALLSSMSAGGWRHKAVIYRTWCKGY--QAL
                                                                                                     GWPFVF
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Similarity 23.2%;
91; Conservative ?
                                                                                                    -----YIFGGVGCVCCLLWFVVIYDDPVSYPW-----ISTSEKEYIISSL
                                -GSSKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSVYHV
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                                                                                                                                                                                                        Score 110.5; DB Pred. No. 0.028; 8; Mismatches 13
-AW--CLA--SYLWPDAVMLVVVGLVLLF----
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Query Match Best Local :

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KW 11-AUG
FT W09521
PN W09521
PN W9521
PN 14-FEE
PR 14-FEE

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NR N-ESDB; 702-17.

NR N-BOB; 703-17.

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                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-FEB-1994;
13-MAY-1994;
29-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_difference 1. .3011

/note= "others correspond to degenerate codons in T04247"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1996 (first entry)
02-JUL-1996 (first entry)
Hepatitis GB virus (HGBV) contig C protein prod.
Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
Hepatitis GB virus; HGBV; diagnosis; treatment; vaccine;
reagents; non-A; non-B; non-C; non-D; non-E; clone; GB contig
reagents; infected plasma; lambda phage; cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buijk SL, Da
Muerhoff AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Simons JN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-1994;
27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09521922-A2
17-AUG-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R95020 standard; Protein; 3011
753 LPFVSMILGLANLVLYFRWMGPQ----RLMFLVLWKLARGAFPLALLMG-ISATRGRTSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R95020;
                                                                           79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 838
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                                                              LPAKSSILG-GQFAIWERWGPPQERSRLCSIALSGMLLGCFTAILIGGFISET-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95-293123/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGLPV----VARRGDEVLIGVFQDVNHLPPGFVPTAPVVIRRCGKGFLGVTKAALTGRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLHPGNVMVLGTATSPSMGTCLNGLLFTTFHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFGWRNVFFLLFAVN-----LIGLLFYLIFG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTV-----SGF-----LLSQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KMCARGAYLFDHMGSFSRAVKERLLEWDAALEPLSFTRTDCRIIRDAARTLSCG---QCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPYLNSGY------
                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABBOTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dawson GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U02118.
US-196030.
US-242654.
US-283314.
US-344190.
US-344185.
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-344557.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                     5.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desai
r IK,
                                                                                                                               Score 108.5; DB 1;
Pred. No. 0.046;
7; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM, Erker JC,
Pilot-Matias TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leary TP;
, Schlauder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTATALLTLSCGLSTLCQ
                                                                                                                                                                                                    Length
                                                                                                                                      Indels 131;
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                                                                                                                                                                                                        3011;
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                                                                                                                               Gaps
   808
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밁 Qy

224

101 ERSRLCSIALSGMLLGCFTAILIGGFISETLG--WPFVFYIF----GGVGCVCCLLWFVV 154

ERGRAMGTALGGLALGLLVGAPFGSVMYEFVGKSAPFLILAFLALLDGALQLCILQPSKV 283

Matches

Conservative

37;

Score 107.5; DB Pred. No. 0.0039; 7; Mismatches 10

100; 1:

Gaps

11;

Length Indels

470; 61;

Query Match Best Local Similarity

5.2%; 24.4%;

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     PT Human amine transporter (HAT), stimulates uptake of produced disease, e.g. Parkinson's or Alzheimer's disease. PT neuro:transmitter(s) - useful for treating and diagnosing neurological disease, e.g. Parkinson's or Alzheimer's disease. PT neurological disease, e.g. Parkinson's or Alzheimer's disease. PT neurological disease. PT neurological disease of produced from cload produced from cload cload (T35417) isolated from cDNA library derived from cDNA cload (T35417) isolated from cDNA library derived from cload cload cload produced from cload sequence was deduced from cload produced from cload sequence was deduced from cload produced from cload produced from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-1996.
01-MAR-1995;
01-MAR-1995;
schizophrenia,
Sequence 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 96-412775/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cao L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human amine transporter.
Amine transporter; neurotransmitter; neurological disease;
Alzheimer disease; Parkinson disease; therapy; diagnosis;
agonist; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R99353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R99353 standard; Protein; 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KMCARGAYLFDHMGSFSRAVKERLLEWDAALEXLSFTRTDCRIIRDAARTLSCG----QCV 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIRDNGLLSALPETVAWVIGMYGGYLADFLLTKKF--RLITVRKIATILGSLPSSALIVS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWPFVF-----YIFGGVGCVCCLLWFVVIYDDPVSYPW-----ISTSEKEYIISSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLHPGNVMVLGTATSRSMGTCLNGLLFTTFHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGIYINVLDIAPRYSSFLMGASR-----GFSSIAPVIVPTV-SGF-----LLSQDP 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GLFDALD----WA-----LEELLVSRPSLRRLARVVECCVMAGEKATTVRLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RQRVVRSPLGEGRPTKPLTI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQQV-----GSSKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSVYHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAEFCFDVTFEVDTSVLGWV-VASVVAWAIALLSSMSAGGWKHKAIIYRTWCKGY--QXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO-U02645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "unidentified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCI
CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC
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Search completed: May 25, 2000, 14:11:15 Job time: 2352 sec

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Total number of hits satisfying chosen parameters:
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           Sequence 1, Appli
Sequence 3, Appli
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US-08-805-118-1
                                                                                               US-08-805-118-1
                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08805118 Patent No. 5985604
                Query Match
Best Local Similarity
Matches 401; Conserv
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APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/805
FILING DATE: Filed Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
REFERENCE/DOCKET NUMBER: PF-0:
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LIBRARY: BRAITUT02
CLONE: 754412
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MEDIUM TYPE: Diskett
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ZIP: 94304
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CITY: Palo Alto
STATE: CA
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TOPOLOGY: 11
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STREET: 3174 Porter Drive
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US-08-663-552-2
PCT-US93-05704-2
US-08-477-451-7
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Patent No. 5432081
Sequence 6, Appli
Patent No. 5268463
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Sequence 9, Appli
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Result No.

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Query Match

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Scoring table: Sequence:

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Post-processing: Minimum Listing

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GENERAL INFORMATION:
GENERAL TOANT: Feder, John N.
Greqc
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                                                         TELEFAX: 415-576-0300 INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Megabase Transcript Map: TITLE OF INVENTION: Sequences and Antibodies NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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TOPOLOGY: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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RESULT 3
US-08-805-118-3
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; LOCATION: 1..480
; OTHER INFORMATION:
US-08-724-394A-11
                                                                                                                                                                                                                                                      Sequence 3, Application US/08805118
Patent No. 5985604
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olja
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 398;
         APPLICATION NUMBER: US/08/80 FILING DATE: Filed Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                              SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                       COMPUTER: IBM COR
OPERATING SYSTEM:
                                                                                                                                                                                      STREET: 3174 POI
CITY: Palo Alto
APPLICATION NUMBER:
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82.9%;
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Pred. No. 1.1e-202;
1; Mismatches 2;
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RESULT 4
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                                                                                                                                                                                           Sequence 9, Application US/08724394A Patent No. 5872237
                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO: 3:
      APPLICANT: Feder, John N.
APPLICANT: Lauer, Peter M.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
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TELEPAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 480 anino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
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MEDIUM TYPE: Floppy disk
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NAME: Fitts, Renee A.
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CITY: San Francisco
STATE: CA
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ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                        76 PKSL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor
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Best Local
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ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Fitts, Renee A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Megabase Transcript Map: TITLE OF INVENTION: Sequences and Antibodies
172 YIISSLKQQVGSSKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSVYHVN 231
                                                                         112
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                                                                                                 128 ISSLLTLFTPLAADFGVILVIMVRTVQGMAQGMAWTGQFTIWAKWAPPLERSKLTTIAGS 187
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                                                                                                                                                                                                                                                      10 RKVPSLCSARYGIALVLHECNFTTIAQNVIMNITMVAMVNSTSPQSQLNDSSSEVLPVDSF 69
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Region LOCATION: 1.470 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/724,394A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                         Local Similarity 38.4 es 161; Conservative
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                                  GSAFGSFIILCVGGLISQALSWPFIFYIFGSTGCVCCLLWFTVIYDDPMHHPCISVREKE
                                                     GMLLGCETAILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKE 171
                                                                                                                                                                   NNSSISIKEFDTKASVYQWSPETQGIIFSSINYGIILTLIPSGYLAGIFGAKKMLGAGLL 127
                                                                                                                                                                                                         GGLSKAPKSLPAKSSI-----
                                                                                                                                                                                                                                     RKGPDFCSLRYGLALIMHFSNFTMITQRVSLSIAIIAMVNTTQQQGLSNASTEGPVADAF 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 amino acids
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Tsuchihashi, Zenta
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Ruddy, David A.
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Best Local Similarity
Matches 112; Conserv
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                                                                    191
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                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (317) 276-0756
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APPLICATION NUMBER: US 0
FILING DATE: 27-APR-1995
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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APPLICANT:
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                            132 GWPEVFYIFGGVGCVCCLLMFVVIYDDPVSYPWISTSEKEYIISSLKQQVGSSKQ---PL 188
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                                                                                                                                   161 IPSAARVHYGCVI-----FVRILQGLVEGVTYPAC-----
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                           TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gaylo, Paul J. REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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GWSSVFYVYGSFGIFWYLFWLLVSYESPALHPSISEEERKYI----EDAIGESAKLMNPL
                                                                                              LSKAPKSLPAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGCFTAILIGGFISETL 131
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    Application US/08647484
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SYSTEM: PC-DOS/MS-DOS
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N: HUMAN BRAIN SODIUM DEPENDENT INORGANIC

OFFINANCE AND RELATED NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                        276-3861
                                                                                                                                                                                                    23.1%; Score 479; DB 1; 28.2%; Pred. No. 2.3e-42; tive 68; Mismatches 155
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                                                                -HGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYS 232
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US-08-647-481-2
US-08-647-481-2
Sequence 2, Application US/08647481
; Patent No. 5618918
; GENERAL INFORMATION:
; APPLICANT: Paul, Steven M.
; APPLICANT: Paul, Steven M.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NU
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                                                                                                              12 VPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDSSEVLPVDSFGG 71
                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
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FILING DATE: 14-MAY-1996
                                                                                                                                                      Local Similarity 28.1 Local Similarity 28.1 Local Similarity
                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
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                  LSKAPKSLPAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGCFTAILIGGFISETL 131
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Lilly Corporate Center
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                                                                                                                                                                    23.1%; Score 479; DB 1; Length 560; 28.2%; Pred. No. 2.3e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Release #1.0, Version #1.30
-HGIWSKWAPPLERSRLATTAFCGSYAGAVVAMPLAGVLVQYS 232
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                                                                                                                                          ; MOLECULE TYPE: US-08-430-033A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08430033A Patent No. 5686266
                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                   TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1076-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ni, Binhui
APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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CITY: Indianapolis
Todiana
    12
                                                                                                                                                                               TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVLAVGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREE
VPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDSSEVLPVDSFGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WRNVFFLLFAVNLLGLLFYLIFGEADVQEWAKERKLT 399
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Lilly Corporate Center
                                       Conservative
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                                                                                                                                                             protein
                                                       23.1%; Score 479; DB 1; 28.2%; Pred. No. 2.3e-42;
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                                       68;
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                                       Mismatches
                                                                          Length 560
                                       Indels
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PCT-US96-05792-2
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                                Best Local Similarity 28.2 Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application:
                                                                Query Match
                                                                                                                                                                                                                    TELEFAX: (317)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                    NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/4:
FILING DATE: APPLI 27, 11
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC TITLE OF INVENTION: PHOSPHATE COTRANSPROTER
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APPLICANT: Paul,
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                                                                                                                                                   TOPOLOGY:
12 VPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDSSEVLPVDSFGG 71
                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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276-3861
270; 2:
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                                                                                                                                                                                                                                                  276-0756
                                                23.1%;
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                                  68;
                             Score 479; DB 4; I
Pred. No. 2.3e-42;
58: Mismatches 155;
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                                                              Length 560;
                               Indels
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US-08-805-118-4
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                                              TOPOLOGY:
                                                                                 TYPE:
                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                           LENGTH:
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Sequence 4, Application US/08805118 Patent No. 5985604
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APPLICANT: Lal, Preetl
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 31/.
CITY: Palo Alto
                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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LIBRARY: GE...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 GWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYIISSLKQQVGSSKQ---PL 188
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                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WQYVFLIASLVHYGGVIFYGVFASGEKQPWAEPEEMS
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
             ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION UMBER: 29,135
REFERRENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Warren, Patrick
TITLE OF INVENTION: NOVEL 7
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Burnham, Martin
APPLICANT: Lonetto, Michael
APPLICANT: Warren, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 WRNVFFLLFAVNLLGLLFYLIFGEADVQEWAKERKLT 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303 LTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDPEFG
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TELEPHONE:
                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVLAVGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREE
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                                                                                                                                                                                                                                                                                                                                          08543
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Lawrenceville
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                                                  GM10044
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Pred. No. 6.1e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 158;
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US-08-898-976-4
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Best Local S
Matches 76
                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08898976 Patent No. 5891670 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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LENGTH: 462 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
COMPUTER READABLE FORM:
MEDIDIM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,976
                                                                                                                                                                                                                                                          APPLICANT: Burnham, Martin
APPLICANT: Lonetto, Michael
APPLICANT: Warren, Patrick
TITLE OF INVENTION: NOVEL TETRACYCLINE
TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                           NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 LNRWTQSEK 462
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                                                                                                                                        COUNTRY:
                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SRGFSSIAPVIVPTVSGFLLSQDP------EFGWRNVFFLLFAVNLLGLLFYLIFGEAD 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGA 335
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                                                                                                                        08543
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76; Conservative
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997 Lenox Drive, Building
                                                                                                                                        USA
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17.7%; Pred. No. 0.0001;
ative 86; Mismatches 158;
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RESULT 13
US-08-466-033-15
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                                                                                                                                                                                                Sequence 15, Application US/08466033 Patent No. 5766840
           APPLICANT: Wages, John
APPLICANT: Young, Lavonne M.
APPLICANT: Fry, Kirk E.
APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Virus an
TITLE OF INVENTION: Cloning Thereof
NUMBER OF SEQUENCES: 277
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kim, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 462 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    404 A---VSVGIAIAAALIDFKALNFPGNDALSSHFG--IILIILGLMSIVGLVLFVI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                       454 LNRWTQSEK 462
                                                                                                                                                                                                                                                                                                                                      389 VQEWAKERK 397
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     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGA 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PFVFYI------FGGVGCVCCLLWFVVIYDDPVSYPWISTS 168
                                                                                                                                                                                                                                                                                                                                                                                                 SRGFSSIAPVIVPTVSGFLLSQDP-----EFGWRNVFFLLFAVNLLGLLFYLIFGEAD 388
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Dehlinger & Associates
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Pred. No. 0.(
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; MOLECULE TYPE:
US-08-466-033-15
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Best Local
                                                                                                                                                                                                                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO:
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LENGTH: 2873 amino aci
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APPLICATION NUMBER: US 08
FILING DATE: 03-AUG-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,886
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 01
FILING DATE: 23-NOV-1994
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FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 26-OCT-1994
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                             693 GAEFCFDATFEVDTSVLGWV-VASVVAWAIALLSSMSAGGWRHKAVIYRTWCKGY--QAI
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                        292 LNSGY---
                                                                                                                                                                                                                                       132 GWPFVF-----
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                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Fabian, Gary REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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CITY: F
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                                                                                   DNGLLSALPFIVAWVIGMVGGYLADFLLTKKF--RLITVRKIATILGSLPSSALIVSLPY 291
                                                   --GLFDALD----WA-----LEEILVSRPSLRRLARVVECCVMAGEKATTVRLVSKMC
                                                                                                                        RQRV--VRSPLGEGRPAKPL----TFAWCLA--SYIWPDAVMMVVVALVLLF-----
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20~MAY-1994
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03-AUG-1994
                                                                                                                                                                                                                              -YIFGGVGCVCCLLWFVVIYDDPVSYPW-----ISTSEKEYIISSL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324-0960
                                                                                                                                                                                                                                                                                                                                      5.1%; Score 106.5; DB 1; 22.9%; Pred. No. 0.078; tive 42; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/344,271
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-ITATALLTLSCGLSTLCQSGI 317
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US-08-638-911A-2
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APPLICANT: Belaey
APPLICANT: Chong,
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 04/24/96
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: EVANS, SUSAN T.
REGISTION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chong, Susan M.
TITLE OF INVENTION: Hepatitis G
NUMBER OF SEQUENCES: 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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  292 LNSGY---
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                                                                            DNGLLSALPFIVAWVIGMVGGYLADFLLTKKF--RLITVRKIATILGSLPSSALIVSLPY 291
                                                                                                                                        KOOVGSSKOPL----PIKAMLRSLPIWSICLGCFSHOWLVSTMVVYIPTYISSVYHVNIR: |: | : | : |: |: : : :
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                                      --GLEDALD----WA-----LEEILVSRPSLRRLARVVECCVMAGEKATTVRLVSKMC
                                                                                                                       RQRV--VRSPLGEGRPAKPL-----TFAWCLA--SYIWPDAVMMVVVALVLLF------
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350 Cambridge Avenue, Suite 250
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-ITATALLTESCGLSTLCQSGI 317
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Patent No. 5
                                  TELEFAX: (4
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APPLICATION NUMBER: US 08/389,886
FILING DATE: 15-FEB-1995
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APPLICATION NUMBER: US 08/344,271
FILING DATE: 23-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Linnen, Jeffrey M.
TITLE OF INVENTION: Hepatitis G Vir
TITLE OF INVENTION: Cloning Thereof
NUMBER OF SEQUENCES: 277
          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           PRIOR APPLICATION DATA:
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                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                               FILING DATE: 20-MAY-1994 ATTORNEY/AGENT INFORMATION:
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                                                                                                REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                               TELEPHONE:
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350 Cambridge Ave., Suite
2873 amino acids
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Young, LaVonne M.
Fry, Kirk E.
                                    (415) 324-09
OR SEQ ID NO:
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                   363 WRNVFFLLFAVN-----LIGLLFYLIFG 385
                                                      898 PV----VARRGDEVLIGVFQDVNHLPPGFVPTAPVVIRRCGKGFLGVTKAALTGRDPDLH 953
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                                                                                                                                               292 LNSGY------ITATALLTLSCGLSTLCQSGI 317
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Search completed: May 25, 2000, 14:25:01 Job time: 2804 sec

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gb_htg6:aC018666

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9b_pat:AR036571
9b_pr3:HSU90545
9b_pr1:AB020527
9b_pr1:AB020527
9b_pr2:HSNAPI1
9b_ro:RU28504
9b_ro:RU28504
9b_ro:RUNAPT1CT
9b_pr1:HUMAPI4
9b_pr1:HUMAPI4
9b_pat:AR036570
9b_pat:AR036570
9b_pr3:HSU90544
9b_ht22:AL138726
9b_pr3:HSZ839737
9b_pr3:HSZ83953
9b_pat:I40028
9b_pat:I40020
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9b_pat:I40220
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Query length: 401
Database: GenEmbl:*
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-Q-/cgn2_l/USPTO_spool/US09391958/runat_24052000_213330_7161/app_query.fasta.1
-DB-GenEmbl -QFWT-fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXY=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -ALIGN=15 -MODE-LOCAL
-OUTFMT=pfs -NORM-ext -MINLEN=0 -MAXLEN=1000000 -USER=US09391958
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
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                    12 | AJ397747 Homo sapiens mRNA for 1 283953 H.sapiens mRNA; clone CI 1 140028 Sequence 1 from patent 16 | 140029 Sequence 1 from patent 16 | 140220 Sequence 1 from patent 16 | 140220 Sequence 3 from patent 16 | 173259 Sequence 3 from patent 16 | 173259 Sequence 3 from patent 16 | 173259 Sequence 3 from patent 173260 Sequence 3 from patent 173260 Sequence 3 from patent 18 | AF095787 Caenorhabditis elegant 18 | AF095787 Caenorhabditis elegant 19 | AF095787 Caenorhabditis melanogas 19 | AF024691 Drosophila melanogas 19 | AC006302 Drosophila melanogas 19 | AC006302 Drosophila melanogas 19 | AC001336 Drosophila melanogas 19 | AC004345 Drosophila melanogas 19 | AC004246 Drosophila melanogas 19 | AC004246 Drosophila melanogas 19 | AC004246 Drosophila melanogas 19 | AC0019866 Drosophila melanogas 19 | AC019866 Drosophila melanogas 19 | AC020165 Drosophila melanogas 19 | AC020165 Drosophila melanogas 19 | AC020165 Drosophila melanogas 19 | AC008232 Drosophila melanogas 19 | AC00832 Drosophila melanogas 19 | AC008434 Drosophila melanogas 19 | AC008434 Drosophila melanogas 19 | AC008448 Drosophila melanogas 19 | AC005463 Drosoph
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Feder, J.Nathan, Kronmal, G.Scott, Lauer, P. Tsuchihashi, Z. and Wolff, R.K.
Megabase transcript map: novel sequences
Patent: US 5872237-A 19 16-FEB-1999;
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                                                                                               ThrSerProGlnSerGlnLeuAsnAspSerSerGluValLeuProValAs
                                                                                                                                                                                       leAlaGlnAsnVallleMetAsnIleThrMetValAlaMetValAsnSer
                                                                                                                                                                                                                                                      pSerPheGlyGlyLeuSerLysAlaProLysSerLeuProAlaLysSerS
                                                                                                                                                              TAGCACAAAATGTCATCATGAACATCACCATGGTAGCCATGGTCAACAGC
                                                                      ACAAGCCCTCAATCCCAGCTCAATGATTCCTCTGAGGTGCTGCCTGTTGA
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Ratio: 5.165
milarity: 99.501
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Submitted (25-FEB-1997) Sequencing, Mercator Genetics, Campbell Avenue, Menlo Park, CA 94025, USA
Location/Qualifiers
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SYPWISTSEKEYIISSKLOQVGSKQDLFIKAMLRSLPIWSICLGGESHQMLVSTMV
YIPTYISSVYHVNIRDNGLLSALPFIVAWVIGMVGGYLADFLLTKKFRLITVWKIATI
IGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTLCQSGYYINULDIAPRYSSFLMG
IGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTLCQSGYYINULDIAPRYSSFLMG
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377. .1582
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/db_xref="taxon:9606"
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                                                                                                             eTyrIleAsnValLeuAspIleAlaProArgTyrSerSerPheLeuMetG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugano, S. and Shibui, A. Direct Submission
Direct Submission
Submitted (27-NOV-1998) to the DDBJ/EMBL/GenBank databases.
Sugano, Institute of Medical Science the University of Tokyo
Department of Vilorogy; 4-6-1 Shirokanedai, Minato-ku, Tokyo
108-8639, Japan (E-mail:ssugano@ims.u-tokyo.ac.jp,
Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens tissue_lib:small intestine cDNA clone:kaia2138.
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Na/PO4 cotransporter homolog
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                             Ratio:
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109. .1602
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651 c 560 g 767 t
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alignment_block: US-09-391-958-1 x AB020527

Similarity:

Percent

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Align seg 1/1

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||||||||||||||||||
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                                                                                                                                                                                                         LeuProIleLysAlaMetLeuArgSerLeuProIleTrpSerIleCysLe 204
                                                                                                                                                                                                                                                                                                                  luTyrIleIleSerSerLeuLysGlnGlnValGlySerSerLysGlnPro ::|||||||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTCCTGACCCTCTTCATTCCACTGGCAGCTAATGCGGGAGTGGCCTTGC 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAATATTTGGAGCCAAGTATGTGGTTGGTGCTTGGTTTATTTCCTC 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATATCTTTGGAGGAATTGGCTGTGCTTGTTGTCCTCTCTGGTTTCCTCT
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REFERENCE
AUTHORS
TITLE
                                                                                                                          COMMENT
                                                                                                                                                                                                                     REFERENCE
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VERSION
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ORGANISM
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LOCUS HSNAPI1
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TITLE
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                                                                                                                                              Direct Submission
Submitted (02-APR-1993)
Institute for Molecular
                                                                                                                                                                                                                                                                     Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1549)
Chong,S.S., Kristjansson,K., Zoghbi,H.Y. and Hughes,M.R.
Molecular cloning of the cDNA encoding a human renal sodium
phosphate transport protein and its assignment to chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSNAPTI 1549 bp mRNA pRI 25-J
H.sapiens mRNA for sodium-phophate transport system 1.
                                                                                                                                                                                                  Chong, S.S
                                                                                                                                                                                                                                                                                                                                                                                                   brush border membrane; NPT1 gene; transporter; transporter.
                                                                                                                                                                                                                                  94117004
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                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       x71355.1 GI:450531
                                                                                                                                    7030, USA
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                                                                                                 Location/Qualifiers
                                                                                                                                             S.S. Chong, Baylor College of
Genetics, One Baylor Plaza, Ho
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                                                                                                                                           Houston,
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                                                                                                                                                            Medicine,
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alignment_block:
US-09-391-958-1 x HSNAPI1
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                                                      86 LeuGlyGlyGlnPheAlaIleTrpGluArgTrpGlyProProGlnGluAr 102
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13. .1416
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401 1412	GlyGluAlaAspValGlnGluTrpAlaLysGluArgLysLeuThrArgLe::: :::: :	385 1363
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1413 C 1413

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BASE COUNT
ORIGIN
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US-09-391-958-1 x RNU28504
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LOCUS RNU28504
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Percent Similarity:
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CDS
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                                                                                                                                                       source
                                                                                                                        18
                                                                                                                                                                           2 GlnValAspGluThrLeuIleProArgLysValProSerLeuCysSerAl 18
                                                                                                 aArgTyrGlyIleAlaLeuValLeuHisPheCysAsnPheThrThrIleA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-JUN-1995) Zijian Xie, Pharmacology, Medical College Ohio, 3000 Arlington Ave, Toledo, OH 43699, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular cloning of two rat Na+/Pi cotransporters: evidence for differential tissue expression of transcripts Cell. Mol. Biol. Res. 41 (5), 451-460 (1995)
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Li,H. and Xie,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNU28504 1700 bp mrNA ROD 11-Apr-199 Rattus norvegicus Na+/Pi cotransporter-1 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Norway rat.
Rattus norvegicus
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68.455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="core sequence common to both isoform-a and soform-b transcripts"
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Rattus.
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	101	OGlnSerGlnLeuAsnAspSerSerGlnValLeu	-4
	Z TAT	ASCUACCCATTATCTAACAAGTCTGTAGCAGAGATGCTGGATAATGT	
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	70	.yG1yL	Ν
	291	CCTGTTGG	40
	73	SerLysAla	ú
	341	AGCATACCCAATGGAGAAAATAATTGGGTCTTCATTGTTC	90
	76	ProLysSerLeuPro8	0
	391	GCTCATCCCACCAGCTGCACAAGTC	40
	81	AlaLysSerSerIl	6
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	120	lalleLeulleGlyGlyPhelleSerGluThrLeuGlyTrpProPheVal 1	36
	ω i	heTyrIlePheGlyGlyValGlyCvsValCvsCvsLeuLeuTrnPheVa 1	2 6
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	37	eGlyMetValG1 2	53
	25.3	77777777777777777777777777777777777777	, ,
9	91	GTCAGATGTCAGACTTCCTCTGTCAAGGAAGATTTTCAGCGTAGTTG 1	
10 2	69	hrValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeu 28	5 5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAGGAGATATTCAGGACTGGGCTAAAGAAACAAAAACCACACGGCTG 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACAGCTTTAATTGGAATATTTGGGGGGCCTAATTTCTTCAACTCTTGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-JAN-1994) Institute for Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning, genetic mapping and expression analysis sodium-dependent phosphate cotransporter Am. J. Physiol. 268, 1038-1045 (1995)
2. (bases 1 to 1885)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euther Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1885)
Chong, S.S., Kozak, C.A., Liu, L., Bordeau, J.E., Hughes, M.R., Kristjansson, K. and Dunn, S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.musculus Npt1 mRNA
X77241
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                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.S. Chong, Baylor College of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                     One Baylor Plaza,
                                                                                                                                                                                                                                                           pSPORT1
                                                                                                                                                                                                                                                           (BRL)
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                                                                                                                                                                                                                                                           plasmid vector"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 CAAATGGAGAACCAGTGCCTCCCCAAGAAAGTTCCAGGGTTCTGTTCCTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GlnValAspGluThrLeuIleProArgLysValProSerLeuCysSerAl 18
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PheTyrIlePheGlyGlyValGlyCysValCysCysLeuLeuTrpPheVa 153
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                                                                                                                                                                                                                                 GlyGlyGlnPheAlaIleTrpGluArgTrpGlyProProGlnGluArgSe 103
                                                                                                                                                                                                                                                                                                                                                                                                  sSerLeuPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerGluValLeuProValAspSerPheGlyGlyLeuSerLysAlaProLy 77
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                                                                                                                                                                                                           ACAGGCCAGCATGAAATATGGGTCAAATGGGCACCTCCCTTAGAACGAGG
                                                                                                                                                                                                                                                                                       TAGTCATTGTGTGTCGAGTACTCCAGGGAATAGCCCAGGGAACAGTGTCA 526
                                                                                                                                                                                                                                                                                                                                                                   CTCTTTGATGTCCTTGCTCATCCCACCTGCTGCACAAGTCGGAGCTGCTT
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GEIQDWAKEIKTTRL"
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FDDFKPHPYMSSSKNYIISSLMQQASGFQSLPFKAMLKSLPJETIRKFAFIWSN
SLLVTYTFFFISTVLHVNYREMGLLSSLPYLLAVICGILAGQNSDFFLTRKFIFSITVL
RKLFTTLGSFCPVIFIMCLLYLSYNFYSTVIFLTLANSTLSFSYCGQLINALDIAPRY
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677

TTCTACATCTTTGGTATTGTTGGGTGTGTTCTGAGTCTTTCCTGGTTCTT 726

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ACCESSION
VERSION
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LOCUS
                                                                KEYWORDS
                                                                                                                                                                                      seq_name: gb_pr1:HUMAPI4
                                                   SOURCE
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                D28532.1 GI:639841
Na/P14; renal Na+-dependent phosphate cotransporter Homo sapiens adult male kidney cortex cDNA to mRNA.
Homo sapiens
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Human mRNA for
                                                                                                            complete cds.
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or renal
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alignment_block:
US-09-391-958-1 x HUMAPI4
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201 AAAGAACCCTATGTATAATTGGAGCCCAGATGTCCAGGGAATCATCTTGA
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                                                                                                                    SerProGlnSerGlnLeuAsnAspSerSerGluValLeu.........
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                                                                                      GATCCACATGGTTTGCCCAACACCTCCACAAAGAAGCTCCTGGATAATAT
                                                                                                                                                                           CACAGCTCATGTGCCTGAACCTCACAATGGTAGTCATGGTGAATAGCACA 150
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Cloning and functional expression of a Na(+)-dependent phos
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Miyamoto, K.-I.
Direct Submission
Submitsion
Submitted (17-FEB-1994) to the DDBJ/EMBL/GenBank databases.
Ken-Ichi Miyamoto, School of Medicine, University of Tokushima, Department of Nutrition; 3 Kuramoto-cho, Tokushima, Tokushima 770, Japan (Tel:0886-33.111(ex.2527), Fax:0886-33-7094)
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NVNSTDPHGLPNTSTKKLLDNIKNPMYNNSDPMGGIILSSTSYGVIIIQVPVQYFSGI
YSTKKMIGFALCLSSVLSLLIPPARAGIQVAMVVVCRANQGAQGIVATAQFEIIYVKWA
PPLERGRLTSMSTSGFLLGPFIVLLVTGVICESLGWPMVFYIFGACCCAVCLLMFVLF
YDDFXDHPCISIGEKEYITSSLYQQVSSSRQSLPIKAILKSLFWHAISIGSFTFFWSH
NIMTLYTPMETISMSLHYNIKENGELSSLFYLFAWICGHLAGQLSDFFLTRNILSVIAV
RKLFTAAGFLLPAIFGVCLPYLSSTFYSIVIFLLLAGATGSFCLGGVFINGLDIAPRY
FGFIKACSTLTGNIGGLIASTLTGLILKQDPESAWFKTFILMAAINVTGLIFYLIVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. 305 (Pt 1), 81-85 (1995)
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/product="renal Na+-dependent phosphate cotransporter"
/protein_id="BAA05888.1"
/db_xref="GI:639842"
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1. .1794
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                                                                uLeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrI 319
                                                                                                  GGTGTCTGCCTGCCTTACCTGAGTTCCACCTTCTACAGCATTGTCATTTT 1100
                                                                                                                                                                 hrValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeu :::||||||||::: ||| ||| ||| ::: :::
                                                                                                                                                                                                                               AGGTCAGTTATCAGACTTCTTCCTGACCAGGAATATTCTCAGCGTAATTG
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ORGANISM
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KEYWORDS
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US-09-391-958-1 x RABRCCTX
                                                                                                                        alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                               ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 1855)
Werner,A., Moore,M.L., Mantei,N., Biber,J., Semenza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane transport protein; renal cortical Na/P-i-cotransporter;
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YDDPKDHPCVSLHEKEXITSSLIQQGSSTRQSLFIKAMIKSLFLWAMISSCCFAYLWTY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="expression in Xenopus laevis oocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="kidney cortex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryctolagus cuniculus
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                                   CCCCAACGTTGATCAACTCCATGCTTCATGTTGACATAAGAGAAACGGG
                                                                                                                                                                              ProLeuProIleLysAlaMetLeuArgSerLeuProIleTrpSerIleCy
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|CTCTGCCCATCAAGGCTATGATTAAGTCTCTTCCACTCTGGGCTATTTC
LeuLeuSerAlaLeuProPheIleValAlaTrpValIleGlyMetValGl
                                                            leProThrTyrIleSerSerValTyrHisValAsnIleArgAspAsnGly 236
                                                                                                                               sLeuGlyCysPheSerHisGlnTrpLeuValSerThrMetValValTyrI 220
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TCCTGCTTGTAACGGGTATCATTTGTGAATCTCTGGGCTGGCCCATGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCCCAGCATGAGATATGGGTCAAATGGGCTCCTCCCTTGGAGCGAGG
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BASE COUNT
ORIGIN
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US-09-391-958-1
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SOURCE
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                                Align seg 1/1
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                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                Quality:
Ratio:
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Megabase transcript map: novel sequences and antibodies t Patent: US 5872237-A 18 16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                            Unknown
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IleargAspAsnGlyLeuLeuSerAlaLeuProPhel	.eProThrTyrIleSerSerVa : ACCAACGTATATCAGTACTCT	:CysLeuGlyCysPheSerHisGln TTCCTGGGTTTTTTCAGCCATTTC	ysGlnProLeuProIleLysAlaMetL ::: :: GACGAGCTGTCCCCATAAAGGCGATGG	leSerThrSerGluLysGluTyrIleIleSerSerLe	YrAspAspProVal ATGATGACCCCATG	PheTyrIlePheGlyGlyValG !TCTACATCTTTGGTAGCACTG	ThrAlaIleLeuIleGlyGlyPheIl ::: :: ATCATCCTCTGTGTGGGGGGGACTAAT	GluArgSerArgLeuCysSerIleAlaLeu 		CGGAGTGATTTTGGTCATCATGGTTCGGACAG:		GGTTTGCTGATCTCTTTCCCTTCTCACCCTCTTTAC/		AAGTGGATATTTAGCAGGGATATTTGGAGCAAAA	TATCATCTTTAGCTCCATCAACTATGG		GATACAAAGGCCTCTGTGTATCAATGG	sSerLeuProAlaLysSerSerIle	TOVALASpSerPheGlyGlyL:::: ::::::::::::::::::::::::::::::	: ::: :: CACTCAGCAGCAAGG	rmetValAlametValAsnSerThrSerProGlnSe	uH1sPheCysAsnPheThrThrIleAlaGlnAsnVal: :	
leValAlaTrpVa :::	TyrhisVala CTCCATGTTA	TrpLeuValSerT TGGTTATGCACCA	ימי ער	uLysGlnGlnVal GGCTCAACAGCCC	SerTyrProTrpI ::: CATCACCCGTGCA	lycysvalcyscy CTGTGTCTGCTG	eSerGluThrLeu ::::: CTCACAGGCCTTG	SerGlyMetLeuL TCAGGGTCAGCAT	luargTrpGlyPr ::: ::: CaaagTgggCTCC	CAGGGCATGGC	:	CACTGGCTGC		LeuGIY AAATGCTTGGTGC	CTCTGAT	:	CCCAGAAACT		SerLy AGCAT	 TATCTAATGC	GlnLeuAs	IleMetAsnIleT :::::: : AGTCTGAGCATTG	:: ::::: TGGCTCTTATCAT
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etics, 4040	Direct Submission Submitted (25-FEB-1997) Sequencing, Mercator Gene Campbell Avenue, Menlo Park, CA 94025, USA	TITLE JOURNAL
, Quintana,L. d,E., Fullan, n,C., eder,J.N.	<pre>2 (bases 1 to 2281) Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quin Ruddy,D.A., Kronmal,G.S., Lee,V.K., Mintier,G.A., Quin Domingo,R. Jr., Meyer,N.C., Basava,A., McClelland,E., Mapa,F.A., Moore,T., Thomas,W., Loeb,D.B., Harmon,C., Tsuchihashi,Z., Wolff,R.K., Schatzman,R.C. and Feder,J</pre>	REFERENCE
litary	A 1.1 megabase transcript map of the human hered hemochromatosis locus Unpublished	TITLE JOURNAL
, Quintana,L., id,E., Fullan,A in,C., 'eder,J.N.	uddy,D.A omingo,R lapa,F.A. suchihasi	AUTHORS
ıta; Mammalia;	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebra Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2281)	SOURCE ORGANISM REFERENCE
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1482		1482 .
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280 1482	PheArgLeuIleThrValArgLysIleAlaThrIleLeuGlySerLeu :::	265 . 1440 T
264 1439	lileGlyMetValGlyGlyTyrLeuAlaAspPheLeuLeuThrLysLys. ::::: :::::: CTGTACAATTTTAGGAGGTCAGCTGGCAGATTTCCTTTTGTCCAGGAATC	248 1 1390 C
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97 691	TyrLeuIlePheGlyGluAlaAspValGlnGluTrpAlaLysGluArgLy 3	381 1642
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541	heLeumetGlyAlaSerArgGlyPheSerSerILe CCTCATGGGAATCTCAAGGGGATTTGGGCTCATC	ن ن
130	GIY11eTYT11eASDValLeuASDI1eA	œ ∓
482		- 00
314	hrAlaLeuLeuThrLeuSerCysGlyLeuSerTh	297
1482		1482
297	yr I	281
280 1482	PheArgLeuIleThrValArgLysIleAlaThrIleLeuGlySerLeu::: ::: ::: :::	265 1440
264 1439	lleglymetvalglyglyTyrLeuAlaAspPheLeuLeuThrLysLys. 	4 0
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1692 CCTTACCCGCCTC 1704

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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-FEB-2000) Sanger Centre, Hinxton. Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 16, 2000 this sequence version replaced gi:6911804.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00595 Length: 20679bp
Contig_ID: 00749 Length: 63415bp
Contig_ID: 01806 Length: 15932bp.
* consists of 5 contigs a 'working draft' sequence. It currently
* consists of 5 contigs The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                       Quality:
Ratio:
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AL138726 AL138726 2 GI:6982716 HTGS_PHASE1; HTGS_DRAFT.
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1 (bases 1 to 140266)
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .140266
                                                                                                                                                                                          Percent Identity: 42.942
                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                        3201 others
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286	276lleLeuGlySerLeuProSerSerAlaLeuI	N
53177	26 GTCAGATAATTTGCGTAGCATACAACAGCCAAAGAATGCATCTCACTGTT	532
275	75	N
275 53227	68 IleThrValargLysIleAlaThr	532
267 53277	S1 etValGlyGlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeu 	533
251 53327	35 snGlyLeuLeuSerAlaLeuProPheIleValAlaTrpValIleGlyM ::	533
53377	26 TGTGGTCTCACTGCCTTTATTATGGTAATTTACTCAATCTTTTCTCTTTA	534
235	35A	N
53427	76 GTATGATTTCAGAATGTCATTATTATTAGTAGTAATTTATCAACAAAAGT	534
234	34	N
53477	26 AGTAGCTTTTCTGGGGTATGATTTAAGAGGTTACTGATTTTCCTAAGAAA	535
234	34	N
53527	76 GAAATGTATTTCTTATTACCAAAAATAATCTAATATTTAATACTCATGCC	535
234	34	2
53577	26 TGCTTGCATGGCTGACCAATTACTCTGCCCTCACTAATCATTCCATCTGA	536
234	34	ν
234 53627	28 yrHisValAsnIleArgAsp	536
w	26 GTTAGTTAGCACAATGGTTGTATACATACCAACTTACATCAGCTCTGTGT	
228	11 pLeuValSerThrMetValValTyrIleProThrTyrIleSerSerValT	N
211 53727	95 ArgSerLeuProIleTrpSerIleCysLeuGlyCysPheSerHisGlnTr 	1 537
194 53777	80GlnValGlySerSerLysGlnProLeuProIleLysAlaMetLeu	1 538
53827	76 GACTAAGTGTGTGAGCATCTGTCGGATTTACCGTTATGACCAGTAAATTT	538
179	79	1
53877	26 GACCTTGTATCTGGATTTTCTTGAGGCCTTAAATCTGGATTTTTAAGGGT	539
179	79	1
179 53927	74 leSerSerLeuLysGln	1 539
174 53977	57 paspProValSerTyrProTrpIleSerThrSerGluLysGluTyrIleI	1 540
54027	76 GAAGGTGTTGGCTGCTGCCTTCTCTGGTTTGTTGTGATTTATGA	540

DR Rotterdam, NETHERLANDS

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seq_documentation_block: LOCUS HSA387747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52926 CTTAGGAAATGAATAAACCATAGGGGAAGAACCACAGATAGACCTGTGGC 52877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52876 CGTTTTTTCAGGTATGTTGAGGAAGGGGTATTGATTTGTCCTCATCCCT 52827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53176 TAATTGGTTTCTTCATTTCCTAGGAAGTCTCCCCTCTTCAGCACTCA 53127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTCACCCACAGTATTCCAGTTTTCTCATGGGAGCATCAAGAGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCAGGGCTGAAGGATACTGTCAAACATCTCTGGATCTAGACCGGAACATT 52677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCATTGAATATACATAGTGCAAGTCCTTTTTGATATAATTGTCTAATTA 52777
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1 (bases 1 to 2512)
Verheijen, F.W., Verbeek, E., Aula, N., Beerens, C.E.M.T.,
Havelaar, M.C., Joosse, M., Peltonen, L., Aula, P., Galjaard, H., Van der Spek, P.J.V.D. and Mancini, G.M.S.

A new gene, encoding an anion transporter, is mutated in sialic
                                      2 (bases 1 to 2512)
Verheijen, F.W.
                                                                                                                           acid storage diseases
                                                                                                                                                                                                                                                                                                         human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                            HSA387747 2512 bp mRNA
Homo sapiens mRNA for sialin
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                                                                                               Genet. 23 (4), 462-465 (1999)
              Submission
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                                                                                                                                                                                  714
                                                                                                                                                                                                                                                                        664 AAAATAGGGGGGAAAATGCTGCTAGGATTTGGGATCCTTGGCACTGCTGT
                                                                                                                                                                                                                                                                                                                                                              614 TTTTTTATGGCTACATCATCACACAGATTCCTGGAGGATATGTTGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 TAAGAAGTACCAATGGGATGCAGAAACTCAAGGATGGATTCTCGGTTCCT: 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            514 GCGTGTCCAGAGCATTCTGCTCCCATAAAAGTTCATCATAATCAAACGGG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    467 ATATGGTAGATTCAAATACAACTTTAGAAGAT...AATAGAACTTCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 TTTCTTCATTGTGTATGCATTACGTGTGAATCTGAGTGTTGCGTTAGTGG
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                     GlnPheAlaIleTrpGluArgTrpGlyProProGlnGluArgSerArgLe
ATGCATGCCATGTGGTCTTCTTGGGCTCCCCCCTCTTGAAAGAAGCAAACT
                                                                                   TTGTACTCAGAGCACTAGAAGGACTAGGAGAGGGTGTTACATTTCCAGCC
                                                                                                                                                                             CCTCACCCTGTTCACTCCCATTGCTGCAGATTTAGGAGTTGGACCACTCA
                                                                                                                                                                                                                    oLysSerLeu.....ProAlaLysSerSerIle.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sAsnPheThrThrIleAlaGlnAsnValIleMetAsnIleThrMetValA 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....PheGlyGlyLeuSerLysAlaPr 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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YLGSWLCMILSGQAAIDMLAKWNFSTLCVRRIFSLIGMIGPAVFLVAAGFIGCDYSLA
VAFLTISTTLGGFCSSGFSINHLDLAPSYAGILLGITNTFATIPGMVGPVIAKSLTPD
NTVGEWQTVFYLAAAINVFGAIFFTLFAKGEVQNWALNDHHGHRH"
1 585 c 566 g 749 t
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LAFFGEFIVYALRVNLSYALVDMYDSNITLEDNRTSKACPEHSAPIKYHHNOJGKKYO
WDAETQGWILGSFFYCYIITOOLPGGYVASKIGGKMLLGFGILGTAVLTLFTPIAADLG
VGPLIVLRALEGLGEGYTFPAMHAMMSSWAPPLERSKLLSISYAGAOLGTVISLPLSG
IICYYNNWTYYFYFFGTIGIFWFLLWIMLVSDTPQKHKRISHYEKEYILSSLRNQLS
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59.868
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/db_xref="taxon:9606"
271. 1758
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/db_xref="GI:6562533"
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REFERENCE AUTHORS

713

663

89

68

89 513 466

416 29

763 85

105

813 88

TITLE

REFERENCE

20047778

AUTHORS MEDLINE JOURNAL KEYWORDS SOURCE ORGANISM

sialin.

ACCESSION

AJ387747

52576

GTCAG 52572 erGln 357

356

52626

52676

339

VERSION

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1311
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                                                                             heAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyGluAla 387
                                                                                                                                               uLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLeuLeup
                                                                                                                                                                                           ACATTTGCCACTATTCCAGGAATGGTTGGGCCCGTCATTGCTAAAAGTCT
                                                                                                                                                                                                                  GlyPheSerSerIleAlaProValIleValProThrValSerGlyPheLe 354
                                                                                                                                                                                                                                                                                        alLeuAspIleAlaProArgTyrSerSerPheLeuMetGlyAlaSerArg 337
                                                                                                                                                                                                                                                                                                                                                                                rLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrIleAsnV 321
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                                                                                                                   GACCCCTGATAACACTGTTGGAGAATGGCAAACCGTGTTCTATATTGCTG 1660
                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCTGGCTTCATTGGCTGTGATTATTCTTTGGCCGTTGCTTTCCTAAC
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KEYWORDS
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AUTHORS
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US-09-391-958-1 x HSZ83953
seq_documentation_block:
                       seq_name: gb_pat:I40028
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                                                                                                                                                      sCysLeuLeuTrpPheValValIleTyrAspAspProValSerTyrProT 164
                                                                                                                                          CTGCCTTCTCTGGTTTGTGATTTATGATGACCCCGTTTCCTATCCAT
                                                                                             GGATAAGCACCTCAGAAAAAGAATACATCATATCCTCCTTGAAACAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.sapiens mRNA; clone 283953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-JAN-1997) Gasparini P., Servizio di Genetica Medica, I.R.C.C.S. - Ospedale CSS Viale Cappuccini, I-71013 San Giovanni Rotondo, Foggia, ITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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Gasparini, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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1 (bases 1 to 570)
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FEATURES
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AUTHORS
TITLE
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ORGANISM
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ACCESSION
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KEYWORDS
       BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                 1932 CTGGAGAGAAGCAGCCGTGGGCAGAGCCTGAGGAGATGAGC 1972
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|1485 TGGTGTCCGCGCTGCCCCACCTGGTCATGACCATCGTGCCCATCGGC 1534
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                                         Patent: US 5618677-A 3 08-APR-1997;
Location/Qualifiers
1. .2716
                                                                                                       1 (bases 1 to 2716)
N1,B. and Paul,S.M.
Human brain sodium dependent inorganic phosphate cotransporter
                                                                                                                                                                                                                                                                    Sequence 3 from patent US 140029
                                                                                                                                                                                            Unknown.
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178 sg :: 1285 gg	5⊌ .	188
189 1335 GC	ProIleLysAlaMetLeuArgSerLeuProIleTrpSerIleCys	203
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220 eP 1435 GC	roThrTyrIleSerSerValT ::::::: : CCGACTACTTCGAAGAAGTGT	237 1484
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1882	TGCCTCCCTGGTGCACTATGGAGGTGTCATCTTCTACGGGGTCTTTGCTT	1931
386		
1932	CTGGAGAGAAGCAGCCGTGGGCAGAGCCTGAGGAGATGAGC 1972	

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N_Geneseq_36:X13233
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Query length: 401
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Query: US-09-391-958-1
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N_Geneseq_36:V43712
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3 ! Streptococcus pneumoniae genc
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GB-C viral genomic sequence. H
GT230 genomic RNA sequence for
GT230 gene cDNA sequence for
Streptococcus pneumoniae genom
Human amine transporter cDNA.
Hepatitis GB virus isolate C l
Fragment of HGBV NS3 genomic i
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Fragment HGJ1737 of a new Hepa
GT110 gene cDNA sequence for d
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Human haemochromatosis
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Fragment HGJ1775 of a new Hepa
Mouse osteoclast transporter [
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US-09-391-958-1 x V43711
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                                                               34 leAlaGlnAsnVallleMetAsnIleThrMetValAlaMetValAsnSer
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                                    TAGCACAAAATGTCATCATGAACATCACCATGGTAGCCATGGTCAACAGC
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Ratio: 5.177
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Percent Identity:

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N_Geneseq_36:T15656
N_Geneseq_36:T94168
N_Geneseq_36:V23083
N_Geneseq_36:T08812
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                                   This sequence encodes the human sodium-dependent phosphate cotransporter (C) (MAPTR) of the invention. NAPTR and agonists of it can be used to treat or prevent disorders associated with decreased phosphate levels, cor prevent disorders associated with decreased phosphate levels (C) cancers of the kidney, disorders of decreased phosphate levels including tumoural calcinosis, osteomalacia, osteoporosis, familial hypophosphatementa, rickets, cysteneuria, nephrocalcinosis, familial hypophosphatementa, rickets, cysteneuria, nephrocalcinosis, familial hypophosphatementa, rickets, cysteneuria, nephrocalcinosis, familial chypophosphatementa, rickets, cysteneuria, nephrocalcinic sis, myophosphate syndrome, myoclonic epilepsy, cellitus, hereditary amyloidosis, myopathies including progressive external ophthalmoplegia, Kearns-Sayre syndrome, myoclonic epilepsy, cencephalopathy, cardiomyopathy, hypokalaemia, Goodpastures syndrome, and cisorders of cell signalling through cAMP, ATP, NADPH and collisorders of cell signalling through cAMP, ATP, NADPH and collisorders associated with increased phosphate. Antagonists or inhibitors of NAPTR may be deministered to a subject to treat or prevent disorders associated with increased phosphate levels, e.g. hypocalciuria, hypocalcaemia, and corporation phosphate regulation in neurons, gastrointestinal tract and liver. The products can also be used for detection, diagnosis and drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human sodium-dependent phosphate cotransporter coding sequence.
Sodium-dependent phosphate cotransporter; human; NAPTR; cancer; myopathy;
cell signalling disorder; phosphate regulation disorder; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human sodium-dependent phosphate co:transporter to develop products for treating e.g. cancers, osteoporosis, Alzheimer's disease, diabetes, encephalopathy, myopathy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9837198-A1.
27-AUG-1998.
24-FEB-1998; U03745.
24-FEB-1997; US-805118
                                                                                                                                                                                                                                                                                                                                                                      hypocalciuria or hypoglycaemia.
Claim 5; Fig 1; 66pp; English.
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SerGlyPheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPh
                                                                                                                          AlaLeuLeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyII 317
                          GAGCATCAAGAGGATTTTCGAGCATAGCACCTGTCATTGTACCCACTGTC
                                        lyAlaSerArgGlyPheSerSerIleAlaProValIleValProThrVal
                                                                            THATATCAATGTCTTAGATATTGCTCCAAGGTATTCCAGTTTTCTCATGG
                                                                                         eTyrIleAsnValLeuAspIleAlaProArgTyrSerSerPheLeuMetG
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                                                                                                                                                                                                                                                                           MetValGlyGlyTyrLeuAlaAspPheLeuLeuThrLySLysPheArgLe
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alignment_block: US-09-391-958-1 x V57910

alignment_scores: Ratio: Percent Similarity:

Quality: 2061.00

5.165 99.501

Percent

Identity: Length:

0 99.252

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seq_documentation_block:
ID V57910; standard; cDNA
AC V57910;
IT V57910; standard; cDNA
AC V57910;
IT V57910; standard; cDNA
AC V57910;
IT V57910; standard; cDNA
AC V57910; standard; cDNA
AC V57910;
IT STANDARD SAPIENS.
ICOST SAPIE
                                               Eclaims 58; Fig 7; 209pp; English.

Chaims 61; Also describe 61; Also describe 7; Algorith 61; Also describe 61; Also descr
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09-APR-1998.
30-SEP-1997; U17658.
30-SEP-1997; US-852495.
07-MAY 1997; US-852495.
01-OCT-1996; US-724994.
(PROG-) PROGENTIOR INC.
Feder JN, Kronmal GS, Laue
Tsuchihashi Z, Wolff RK;
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Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE; diagnosis; iron metabolism; NPT3; NPT4; RORet; BTF1; BTF2; BTF3; BTF5; milk protein; lupus; Sjogren's syndrome; hypophosphatemia;
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seq_documentation_block:
ID V57909 standard; CDNA
AC V57909;
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DE Human haemochromatos!
KW Bovine butyrophilin;
KW Homo sapiens. Locat
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Bovine butyrophilin; BT; human hereditary haemochromatolism; NPT3; NPT4; RoRet; BTF1; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; type 1 sodium transport gene: ss.
Claim 52; Fig 7; 209pp; English.

The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. Also described is a method to determine the presence or absence of the common hereditary haemochromatosis (HFE) gene mutation in an individual comprising:

(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA from the individual; and (b) assessing the the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a RoRet gene
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alignment_scores:
Quality:
Ratio:
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US-09-391-958-1 x V57909
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Ratio: 3.305
Percent Similarity: 59.873
940
                                                                                                                                                                                        840 ACTTCGGAGTGATTTTGGTCATCATGGTTCGGACAGTCCAGGGCATGGCC 889
                                                                                                                                                                                                                                                                                      790 TGGTTTGCTGATCTCTTCCCTTCTCACCCTCTTTACACCACTGGCTGCTG 839
                                                                                                                                                                                                                                                                                                                                            740
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                                                                                                                                                                                                                                                                                                                                                                                                                                 590 TCCACTGAGGGGCCTGTTGCAGATGCCTTCAATAACTCCAGCATATCCAT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can similarly be used for hypophosphatemia. The present sequence encodes NTP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 oLysSerLeuProAlaLysSerSerIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ArgLysValProSerLeuCysSerAlaArgTyrGlyIleAlaLeuValLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCACTTGAACGAAGCAAGCTCACCACCATTGCAGGATCAGGGTCAGCAT
                                                                                                                                                        oProGlnGluArgSerArgLeuCysSerIleAlaLeuSerGlyMetLeuL 115
                                                                                                                                                                                                                                                                                                                                     CCAAGTGGATATTTAGCAGGGATATTTGGAGCAAAAAAATGCTTGGTGC 789
                                                                                                                                                                                                                                                                                                                                                                                  AGGGTATCATCTTTAGCTCCATCAACTATGGGATAATACTGACTCTGATC 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerSerGluValLeuProValAspSerPheGlyGlyLeuSerLysAlaPr 76
                                                                                                                                                                                                                                                                                                                                                             .....LeuGly.. 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2281 BP;
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Gaps: 4
Percent Identity: 41.826
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ter cDNA;	JAN-1997 (first entry) an brain Na+ dependent inorganic phosphate cotranspor in sodium-dependent inorganic phosphate cotransporter	30- Huma Bra
	cumentation_block: 42064 standard; cDNA; 2716 BP. 42064.	
	: N_Geneseq_36:T42064	_name
	sLeuThrArgLeu 401 CTTACCCGCCTC 1704	397 1692
397 1691	TyrLeuIlePheGlyGluAlaAspValGlnGluTrpAlaLysGluArgLy 3	381 1642
380 1641	rgAsnValPhePheLeuLeuPheAlaValAsnLeuLeuGlyLeuLeuPhe	364 1592
364 1591	lProThrValSerGlyPheLeuLeuSerGlnAspProGluPheGlyTrpA :::::: ::: TTCCACTGCCACTGGATTCCTCATCAGTCAGGATTTTGAGTCTGGTTGGA	347 1542
347 1541	PheLeuMetGlyAlaSerArgGlyPheSerSerIleAlaProValIleVa	woω
330 1491	InSerGlyIleTyrIleAsnValLeuAspIleAlaProArgTyrSerSer ::: TATGCAAGT	314 1483
1482		1482
314	$\tt eThrAlaThrAlaLeuLeuThrLeuSerCysGlyLeuSerThrLeuCysG$	297
1482		1482
297	ProSerSerAlaLeuIleValSerLeuProTyrLeuAsnSerGlyTy	281
280 1482	5PheArgLeuIleThrValArgLysIleAlaThrIleLeuGlySerLeu ::: :::	265 1440
264 1439	111eG1yMetValGlyG1yTyrLeuAlaAspPheLeuLeuT 	248 1390
248 1389	2 IleArgAspAsnGlyLeuLeuSeralaLeuProPheileValAlaTrpVa :: ::: :::	23; 134(
231 1339	5 hrmetValValTyrileProThrTyrileSerSerValTyrHisValAsn ::::::::: :	215 1290
215 1289	AC - 0	19 124
198 1239	2 GlySerSerLysGlnProLeuProIleLysAlaMetLeuArgSerLeuPr::: ::: :::	18 119
181 1189	- leserIntserdulysGluTyrIleIleSerSerLeuLysGlnGlnVal ::: ::: ::: TAAGTGTTAGGGAAAAGGAGCACATCCTGTCCTCACTGGCTCAACAGCCC	1140

Sec ID AC AC DT DE KW KW KW FH FH

Homo sapiens. Key cds

Location/Qualifiers 461. .2143

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alignment_block:
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Claim 3; Page 57-59; 68pp; English.

Claim 3; Page 57-59; 68pp; English.

Claim 4; Page 57-59; 68pp; English.

Claim 5; Page 57-59; 68pp; English.

Claim 5; Page 57-59; 68pp; English.

Claim 6; Page 57-59; 68pp; English.

Claim 6; Page 57-59; 68pp; English.

Claim 6; Page 57-59; 68pp; English.

Claim 7; Page 57-59; 68pp; English.

Claim 6; Page 57-59; 68pp; English.

Claim 6; Page 57-59; 68pp; English.

Claim 7; Page 57-59; 68pp; English.

Claim 8; Page 57-59; 68pp; English.

Claim 8; Page 57-59; 68pp; English.

Claim 8; Page 57-59; 68pp; English.

Claim 9; Page 57-59; 68pp; Fage 6; Page 6; P
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31-OCT-1996.
25-APR-1996; U05792.
27-APR-1995; US-430033.
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        162
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N1 B, Paul SM;
WPI; 96-497773/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; W05148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 ValProSerLeuCysSerAlaArgTyrGlyIleAlaLeuValLeuHisPh ::::|||||| ::::
                                                                                                                                                                                                                                                    alAlaMetValAsnSerThrSerProGlnSerGlnLeuAsnAspSerSer 61
TyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLy 178
                                                                                    TCTTCTGGTACCTGTTCTGGCTGCTCGTCTCCTACGAGTCCCCCGCGCTG 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSe 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGGGCCCCACCCTTAGAACGGAGTCGCCTGGCGACGACAGCCTTTTGT 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rLeuProAlaLysSerSerIleLeuGlyGlyGlnPheAlaIleTrpGluA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluValLeuProValAspSerPheGlyGlyLeuSerLysAlaProLysSe 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eCysAsnPheThrIleAlaGlnAsnValIleMetAsnIleThrMetV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCCCCTCAGCTGCCCGCGTCCACTATGGCTGTGTCATC.....
                                                                                                                                                                ysValCysCysLeuLeuTrpPheValValIleTyrAspAspProValSer
                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTCCTATGCTGGGGGGGGTCGTCGCGGATGCCCCTCGCCGGGGTCCTTGT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rgTrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 111
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/product-
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2.056
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Gaps:
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seq_documentation_block:
ID V33503 standard; cDNA; 2716 BP
AC V33503;
DT 18-JAN-1999 (first entry)
DE Human sodium-lithium countertr
KW Sodium-lithium countertransport
KW BNP1; human; lithium therapy;
OS HOMO sapiens.
FH Key Location/Quali
FT CDS 461. 2143
FT CDS 461. 2143
FT W09838203-A1.
                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:V33503
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                                                                                                                                                                                                                                                                                                                                                                                                           1932 CTGGAGAGAAGCAGCCGTGGGCAGAGCCTGAGGAGATGAGC 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1832 GCCATGACTAAGCACAAGACTCGGGAGGAGTGGCAGTACGTGTTCCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270
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                                                                                                                            18-JAN-1999 (first entry)
Human sodium-lithium countertransporter BNPI DNA.
Sodium-lithium countertransporter; sodium-phosphate
BNPI; human; lithium therapy; manic depression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        319 eAsnValLeuAspIleAlaProArgTyrSerSerPheLeuMetGlyAlaS 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 leValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 GlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeuIleThr..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTTGGTGGTCGGCTACTCGCACTCCAAGGGCGTG...GCCATCTCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erArgGlyPheSerSerIleAlaProValIleValProThrValSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrIl 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTGCGCAAGTTGATGAACTGCGGAGGCTTCGGCATGGAAGCCACGCTGC 1634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euLeuSerAlaLeuProPheIleValAlaTrpValIleGlyMetValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ProIleLysAlaMetLeuArgSerLeuProIleTrpSerIleCys 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .ValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeuI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCAGATCGCGGACTTCCTGCGGAGCCGCCGCATCATGTCCACCACCAA 1584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuGlyCysPheSerHisGlnTrpLeuValSerThrMetValValTyrIl 220
                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369
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alignment_scores:
Quality:
Ratio:
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US-09-391-958-1 x V33503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PT New isolated lithium-sodium counter-transporter DNA - used to develop products for evaluating lithium-sodium transport in PT erythrocytes, particularly for lithium therapy in manic depression. PS Claim 7; Page 48-50; 64pp; English.

CC countertransporter (LSCT) BNPI (see W70500). LSCTs provide the CC physiological mechanism for the extrusion of lithium from cells, cc i.e. they regulate the cell concentration of lithium. LSCT activity CC determines the therapeutic effect of lithium. The invention provides a simple molecular biological test for the ability of cells to extrude lithium. LSCTs have significance for cells to extrude lithium. LSCTs have significance for cells to extrude lithium. LSCTs have significance for cells to including manic depressives, to treatment with lithium salts. Probes and primers for BNPI, piT-1 (see V33501), PiT-2 (see V33502) can be used in diagnostic tests useful for genetic screenings to predict whether a patient will respond to lithium cumborns. The test is also a screen for susceptibility to, and extent of, manic depressive illness, and is suitable for screening contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: V33503 from: 1 to: 2716
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                                                                                                                                                     1097
                                                           1147 GCAGTACTCAGGATGGAGCTCTGTTTTCTACGTCTACGGCAGCTTCGGGA 1196
                                                                                                                                                                                                                           1047 AATGGGCCCCACCCTTAGAACGGAGTCGCCTGGCGACGACAGCCTTTTGT 1096
                                                                                                                                                                                                                                                                                                                    1031
                                                                                                                                                                                                                                                                                                                                                                                                   1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1023 CCGCCTGC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-1998.
11-FEB-1998, U02875.
27-FEB-1997; US-039462.
(UYEM-) UNIV EMORY.
Gunn RB, Timmer RT;
WPI; 98-520759/44.
                                                                                128 rGluThrLeuGlyTrpProPheValPheTyrllePheGlyGlyValGlyC::: |||||
                                                                                                                                                                      112 GlyMetLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSe 128
145 ysValCysCysLeuIrpPheValValIleTyrAspAspProValSer 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             941
                                                                                                                                                                                                                                                  78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 alAlaMetValAsnSerThrSerProGlnSerGlnLeuAsnAspSerSer 61
                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 ValProSerLeuCysSerAlaArgTyrGlyIleAlaLeuValLeuHisPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; W70500
                                                                                                                                          GGTTCCTATGCTGGGGGGGTGGTCGCGATGCCCCTCGCCGGGGTCCTTGT 1146
                                                                                                                                                                                                                                                                                                                                                rLeuProAlaLysSerSerIleLeuGlyGlyGlnPheAlaIleTrpGluA 95
                                                                                                                                                                                                                                                                                                                                                                                                                               GluValLeuProValAspSerPheGlyGlyLeuSerLysAlaProLysSe 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eCysAsnPheThrThrIleAlaGlnAsnValIleMetAsnIleThrMetV 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCCCCTCAGCTGCCCGCGTCCACTATGGCTGTGTCATC.....
                                                                                                                                                                                                                                                                                                                                                                                      .....TTCGTGAGGATCCTGCAGGGGTTGGTAGAGGGGGGTCACATACC 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2716 BP;
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2.056
58.690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity:
                                                                                                                                                                                                                                                                                                            .......CATGGGATCTGGAGCA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 853 · C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             739 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1030
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PN S KW DE ACC

Sodium-dependent phosphate cotransporter coding sequence fragment.
Sodium-dependent phosphate cotransporter; human; NAPTR; cancer; myopathy;
cell signalling disorder; phosphate regulation disorder; therapy; ss.
Homo sapiens.
W09837198-A1.

seq_documentation_block:

V43712 standard; DNA; V43712; 30-NOV-1998 (first entry)

272 BP

	N_Geneseq_36:V43712	eq_name:
	luAlaAspValGlnGluTrpAlaLysGluArgLysLeuThr 399 ::::::: :: :::::::::::::::	386 1932
386 1931	uLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyG 3: ::: :::	369 1882
369 L881	PheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLe 3 ::: :::::	353 1832
352 1831	erArgGlyPheSerSerIleAlaProVallleValProThrValSerGly 3 :::	336 1782
336 1781	yAlas CATCT	319 1732
319 1731	LeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrIl ::: ::: ::: ::: ::: ::: ::: ::: CTGGTCCTAGCCGTGGGCTTCAGCGGCTTCGCCATCTCTGGGTTCAACGT	303 1682
302 1681	leValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeu :::::	286 1635
286 1634	.ValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeuI :::::: : CGTGCGCAAGTTGATGAACTGCGGAGGCTTCGGCATGGAAGCCACGCTGC	270 1585
269 1584	GlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeuIleThr ::: :::::::::	254 1535
253 1534	euLeuSerAlaLeuProPheIleValAlaTrpValIleGlyMetValGly ::: ::: GTGTCCGCGCTGCCCCACCTGGTCATGACCATCGTCCTGCCCATCGGC	237 1485
237 1484	eProThrTyrIleSerSerValTyrHisValAsnIleArgAspAsnGlyL 	220 1435
220 1434	LeuGlyCysPheSerHisGlnTrpLeuValSerThrMetValValTyrI1 ::::: :::::	204 1385
203 1384	ProlleLysAlaMetLeuArgSerLeuProlleTrpSerlleCys	189 1335
188 1334	SGlnGlnValGlySerSerLysGlnProLeu	178 1285
178 1284	TyrProTrplleSerThrSerGluLysGluTyrIleIleSerSerLeuLy ::: :: :::: CACCCCAGCATCTCGGAGGAGGAGGCGCAAGTACATC	162 1247
1246	TCTTCTGGTACCTGTTCTGGCTGCTCGTCTCCTACGAGTCCCCCGCGCTG	1197

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seq_documentation_block:
ID V57926 standard; DNA; 235033
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                                                                                                                                                                          seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cc sodium-dependent phosphate cotransporter (NAPTR) of the invention. NAPTR cand agonists of it can be used to treat or prevent disorders associated cwith decreased phosphate levels, e.g. cancers of the kidney, disorders of cdecreased phosphate levels including tumoural calcinosis, osteomalacia, consteoporosis, familial hypophosphatemia, rickets, cysteneuria, conseporosis, familial hypophosphatemia, rickets, cysteneuria, conseporosis, familial hypophosphatemia, rickets, cysteneuria, conseporosis, glomerulonephritiis, renal calculus, Alzheimer's conseporosis, elilitus, hereditary amyloidosis, myopathies including progressive external ophthalmoplegia, Kearns-Sayre syndrome, myocionic cepilepsy, encephalopathy, cardiomyopathy, hypokalaemia, Goodpastures considered, encephalopathy, cardiomyopathy, hrough camp, ATP, NADPH and consecutive, encephalopathy, hypokalaemia, Goodpastures considered to a subject to treat or prevent disorders associated with increased phosphate levels, e.g. hypocalcinia, hypocalcaemia, and considered considered to a subject to treat or prevent disorders associated with increased phosphate regulation in neurons, gastrointestinal tract and considered to treat considered to treat or prevent disorders associated with increased phosphate regulation in neurons, gastrointestinal tract and considered to treat considered to treat considered to treat considered to the considered to treat considered to the considered to the considered to treat or prevent disorders associated with considered to the considered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 5.094 Percent Similarity: 100.000
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24-FEB-1997; US-805118.
24-FEB-1997; US-805118.
(INCY-) INCYTE PHARM INC.
Bandman O, Lal P;
WPI; 98-467561/40.
New isolated human sodium-dependent phosphate co:transporter - use to develop products for treating e.g. cancers, osteoporosis, alzheimer's disease, dilabetes, encephalopathy, myopathy, hypocalciuria or hypoglycaemia.
Example V; Page 47; 66pp; English.
This sequence represents a fragment of the DNA encoding the human incompanies of the content of the invention.
                                                                                                                                                                                                                                                                        400
                                                                                                                                                                                                                                                                                                                                                                      383
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Hereditary haemochromatosis subregion from an unaffected individual. Bovine butyrophilin; BT; human hereditary haemochromatosis; HFE;
                                             v57926;
23-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tGlyAlaSerArgGlyPheSerSerIleAlaProValIleValProThrV
                                                                                                                                                                                                                          GTTTA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PhePheLeuLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAGCATCAAGAGGATTTTCGAGCATAGCACCTGTCATTGTACCCACTG
                                                                                                                                                                       N_Geneseq_36:V57926
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                                                                                                                                                                                                                                                                     401
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5.094
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Gaps:
Percent Identity:
                                                                                                   ВP
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6
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100.000
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alignment_block:
US-09-391-958-1 x V57926
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Quality:
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(a) providing DNA or RNA from the individual; and (b) assessing the DNA or RNA for the presence or absence of a haplotype or genotype where the presence or absence of the haplotype genotype indicates the likely presence of the HFE gene mutation in the genome of the individual. The HFE gene sequences from the present invention can be used to develop products for use in the diagnosis and treatment of HFE. The present invention also describes BTF genes, which are homologues of the milk protein butyrophilin (BT), and can be used in the production of agonists and antagonists of BT function. Also described are: (1) a ROREt gene which can be used to develop products for the study, diagnosis and treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes which are homologues of a type 1 sodium transport gene, and can similarly be used for hypophosphatemia.

Sequence 235033 BP; 68786 A; 48466 C; 49441 G; 68340 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                  217123 TTTTATCCCTTCTTCCCAGGTAGCACTGGCTGTGTCTGCTGTCTCCTATG
                                                                                                                                                                                                                                                           217223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; iron metabolism; NPT3; NPT4; RoRet; BTF1; BTF4; BTF5; milk protein; lupus; Sjogren's syndrome; type 1 sodium transport gene; ss. Homo sapiens.
W09814466-A1.
                                                                                                                                                                                                                                                                                                    168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes hereditary haemochromatosis gene products from the human haemochromatosis gene. The present sequence represents a hereditary haemochromatosis subregion from an individual unaffected by hereditary haemochromatosis (HH). Also described is a method to determine the presence or absence of the common hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1997; U17658.
07-MAY-1997; US-852495.
01-OCT-1996; US-724394.
(PROG-) PROGENTIOR INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hereditary haemochromatosis gene products - used to develop products for the diagnosis and treatment of hereditary disorders in iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feder JN, Kronmal GS, La
Tsuchihashi 2, Wolff RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; F1g 8; 209pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism
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                                                                                                                                                                                                                                                       TTCTTTTCAGCCCAGTTCTCCTGGACGAGCTGTCCCCCATAAAGGCGATGG
                                                                                                                                                                                                                                                                                erGluLysGluTyrIleIleSerSerLeuLysGlnGlnValGly.....
                                                                                                                                                                                                                                                                                                                                                                     pPheValValIleTyrAspAspProValSerTyrProTrpIleSerThrS
||||:::||| ||||||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheTyrIlePhe.....GlyGlyValGlyCysValCysCysLeuTeuTr
                                                                                   CTCTGAGAGGCACCATCTTGGCTGCTCTAATACTCATGCTGATTAGATCT
                                                                                                                       rSerLysGln..Pro.....
                                                                                                                                                                      CCTTGTACCTGTGGCCCATGCAGAGGTCTCTAGGGCAGGGTGTGGATCTC
                                   .....LeuProIleLysAlaMetL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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1.975
29.650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 543
Gaps: 9
Percent Identity: 20.994
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hypophosphatemia;
                                          194
                                                                                                                                                                                                                                                                                                    182
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217422
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                                                                                                                                                                      217322
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38	235AsnGlyLeuLeu 2
218322	218273 GGGTAAGTTAATGGCTGGTCTGTGTAACTGACAAATTTTGGTGCTAACGT 2
234	234 2
218272	218223 AGTGTGAAAAAGGATGCTAATTTTCCCCCCAAACAACCACCCAC
234	234 2
218222	218173 GCCCAGAGTGATGCAGCTTCTGGCCCTCTTATCTGAGACAGTGTTCTTTT 2
234	234
218172	GA
234	
218122	GAC
234	234
218072	218023 CAGGAGGCTGAGACAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCA
234	234
218022	217973 ATACAAAAATTAGCCAGGTGTGGTGGCAGGCACCTGTAATCCCAGCTATT:
234	234
217972	217923 ATGCAAGACCAGCCTGACCAATATGGTTTACTAAATATCATCTACTAAAA
234	234
217922	217873 GTAATTCCAGCACTTTGGGAGGCCGAGGCAGGCAGATCATGAGGTCAGGA
234	234
217872	217823 AGCTTCTTTTAGAAATAATATTGCTGGGCCAGGCATGGTGGCTCATGCCT
234	234
217822	217773 CATCCATATTCTTAACCACTATGCTATACTACCACCACCCAGCTGATTCCAA
234	234
217772	217723 GAGATAACTTGCCCCAGGTTGCACAATACTAAGTGATAGAGCTGCTGCAG
234	234
217722	217673 CATTGTTATAATTCCCTTTTCACAGATGTGGAAACAGGACACTTAGAGGT
234	234
217672	217623 GGCTTTACATATAACCATTAATTTAACCTTCACAATGACCTTGAGAGAGG
234	234
217622	217573 AATGATAATGGTAATAAGGAGAAACAGTTCTGTGTTACCTATTACATTCT
234	234
217572	217523 GCTCCATGTTAACATCAGAGATGTGAGTTTACTTCCTATACTTCTACGAA
234	227 lTyrHisValAsnIleArgAsp
227 217522	211 TrpLeuValSerThrMetValValTyrIleProThrTyrIleSerSerVa
217472	217423 TCACATGCCTACCACTTTGGGCCATTTTCCTGGGTTTTTTCAGCCATTTC
210	194 euArgSerLeuProIleTrpSerIleCysLeuGlyCysPheSerHisGln

218323 ANCTOCHANANCTACTOCHANAACTTCCTTCAGAGGTGAGTTCTC 218372 239 SILLIALEMPOOPHALIAVALATTYVALIAGAGGTCAAGGTCAAGGTCAAGGTCAAGTTTAGAAGGTCA 218472 218273 TCCTCCCTTCCTTTTATTCCTCCTGCAGGTCAAGTTTAGAAGTTTAGAAGGTCA 218472 218273 TCCTCCCTTCCTTTTTTTCCCGCAGGTCAAGGTCAAGTTTAGAAGTTTAGAAGGTCA 218472 218273 TCCTCCCTTTTTTTTCCTGCAGGAAGTCTCTCAGAGTTGACCCTTTAGCAGGTCA 218472 218273 CCTCGCAGGTTTCCTTTTGTCAGGAGGTCAAGGTCAAGGTCAAGGTCAAGGTCAAGTTTAGCAGGTCA 218472 271 rgiysilalatfitlichichigysen. Low
to kan a gan a

219790 GCTCCATGTTAACATCAGAGATGTGAGATTTACTTCCTATACGAA 219839 234	euArgSerLeuProlleTrpSerIleCysLeuGlyCysPheSerHisGln::: ::: ::	219490 GGGAAAAGGACCATCCTGTCCTCAACTGGCTCAACAGGTGTGCACA 219539 183	t_block: 91-958-1 x v57903 91-958-1 x v57903 from: 1 to: 237326 eg 1/1 to: v57903 from: 1 to: 237326 PheTyrIlePheGlyGlyValGlyCysValCysCysLeuLeuTr	CC protein butyrophilin (BT), and can be used in the production of agonists CC and antagonists of BT function. Also described are: (i) a RoRet gene CC which can be used to develop products for the study, diagnosis and CC treatment of lupus and Sjogren's syndrome; and (2) NPT3 and NPT4 genes CC which are homologues of a type 1 sodium transport gene, and can CC similarly be used for hypophosphatemia. SQ Sequence 237326 BP; 69596 A; 48904 C; 48217 G; 70609 T; alignment_scores: Quality: 318.00 Length: 543 Ratio: 1.975 Gaps: 9 Percent Similarity: 29.650 Percent Identity: 20.994
271 rgLysileAlaThrIleLeuGlySer.Leu	235	220390 TCCGTTTCAAAAACAAAAAACCCAAGAAATTAATATTGCTTTTATCTGGA 220439 234	234	220040 CATCCATATTCTTAACCACTATGCTATACTACCACCAGCTGATTCCAA 220089 234

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seq_documentation_block:

ID T62652 standard; cDNA to mRNA; 18
AC T62652;
DT 15-MAY-1997 (first entry)
DE DNA encoding protein involved in cephalosporin C; biosynthesis; fe Acremonium chrysogenum.

FH Key 127...1575
FT 199009966-A. Location/Qualifie 127...1575
FT 20009966-A. Location/Qualifie 127...1575
FT 200-1995; J7-167461.
PR 3-JUL-1995; J7-167461.
PR (ASAH ) ASAHI KASEI KOGYO KK. PP: 97-126424/12.
DR WPI; 97-126424/12.
DR WPI; 97-126424/12.
DR Acremonium chrysogenum gene involved to improve chrysogenum
PS Claim 3; Page 9-11; 21pp; Japanes Chrysogenum 201 protein involved in Sequence for a protein involved in Sequence for a protein involved in CC The gene involved in biosynthesis can be used to improve the fermen 201 chrysogenum.

SQ Sequence 1840 BP; 346 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-391-958-1 x T62652
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Claim 3; Page 9-11; 21pp; Japanese.
This cDNA, derived from Acremonium chrysogenum, contains a coding sequence for a protein involved in biosynthesis of cephalosporin (The gene involved in biosynthesis of cephalosporin C or its cDNA can be used to improve the fermentation ability of Acremonium
       625
                                           102 ArgSerArgLeuCysSerIleAlaLeuSerGlyMetLeuLeuGlyCysPh 118
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                                                                                                                                                                                                                                                                                                                                                                                         437 CCGAGATGTACGGCCGCCTCATCCCCTACCATGTCACCAACGTCCTCTTC
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chrysogenum.
1840 BP;
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337 ATCGTCGACTTTGACAGCAGCAGCAGCATCCTCAGCTCTCATCGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 TGTGTACAATGTCGGCCTGGCCATCGGCCCCTTGATCGTGGCGCCCCTTGT 436
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                                                                                           TGATGACCATTGGCGGTGCCACCGTCGCCGATCTTTTTATCCAGGAGGAG
                                                                                                                                                                                        CCCCGCCTTGTCATCTTCCGTATGCTGGCCGGCATGGAGGCTTCTGCCG 574
CGCGGTCGGGCCATTGGCCATTTGGACGTTTGGCCCCGTTGATGGGTCCTGC
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0.809
51.264
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127. .1575
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Gaps: 24
Percent Identity: 23.678
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  674
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372 1490	SerGlnAspProGluPheGlyTrpArgAsnValPhePheLeuLeuPheAl::: :::::::::::::::::::::::::::::::::	356 1 44 1
355 1440	heSerSerIleAlaProValIleValProThrValSerGlyPheLeuLeu:	339 1394
339 1393	<pre>uMetGlyAlaSerArgGlyP ::::: ::: ATTGGCCGCCGCCACCATCC</pre>	322 1344
322 1343	eTyrIleAsnValLe ::: :::: ACAGGTCTACCTTGT	306 1303
305 1302	ACAAGCTCCACTGGATGATGCCCATCTGTGCGACGTCGCTCCTCGGCATT	299 1253
298 1252	euProTyrLeuAsnSerGlyTyrIleThr :: ::::: ::: !TGTGTTTCTTCATCTACGGCTGGGCGACCTACT	283 1203
283 1202	LeuIleThrValArgLysIleAlaThrIleLeuGlySerLeuProSerSe :::	267 1183
266 1182	heLeuLeuThrLysLysPheArg ::: :::	259 1133
259 1132	eIleValAlaTrpValIleGlyMetValGlyGlyTyrLeuAlaAspP: ::::::	243 1083
243 1082	ValTyrHisValAsnIleArgAspAsnGlyLeuLeuSerAlaLeuProPh::: ::: :::	227 1036
226 1035	InTrpLeuValSerThrMetValValTyrIleProThrTyrIleSerSer	210 995
210 994	uProIleTrpSerIleCysLeuGlyCysPheSerHisG ::: ::: 	197 946
197 945	ProIleLysAlaMetLeuArgSerLe	189 898
188 897	ysGlnProLeu	185 853
185 852	rGluLysGluTyrIleIleSerSerLeuLysGlnGlnValGlySerSerL:::: ::::: :::: :::: :::: :::: ::::	168
168 815	PheValValIleTyrAspAspProValSerTyrProTrpIleSerThrSe	152 775
151 774	heValPheTyrIlePheGlyGlyValGlyCysValCysCysLeuLeuTrp :: :::::	135 725
135 724	eThrAlaIleLeuIleGlyGlyPheIleSerGluThrLeuGlyTrpProp::::::	118 675

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alignment_block:
US-09-391-958-1 x T62653
                                                                                                                                                                                                                                                 alignment_scores:
Quality:
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Percent Similarity:
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14-JAN-1997; 167461.
03-JUL-1995; JP-167461.
03-JUL-1995; JP-167461.
(ASAH) ASAHI KASEI KOGYO K
WPI; 97-126424/12.
P-PSDB; W14439.
                                                  1412
                                                                                                    1364 GCCTCATCCCTACCATGTCACCAACGTCCTCTTCGTCCTCTTCACCA..
1452 CTTCCGTATGCTGGCCGGCATGGAGGCTTCTGCCGTGATGACCATTGGCG
                                                                                                                                                                                                                                                                                                                      chrysogenum
Claim 4; Page 11-14; 21pp; Japanese.
Claim 4; Page 11-14; 21pp; Japanese.
This DNA, derived from Acremonium chrysogenum, contains a coding sequence for a protein involved in biosynthesis of cephalosporin The gene involved in biosynthesis of cephalosporin C or its cDNA can be used to improve the fermentation ability of Acremonium
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                                                                                                                                                                                                                                                                                                    can be chrysogenum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
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Key Locatio
exon 935. .1
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               83 erSerIle.LeuGly......GlyGlnPheAlaIleTrpGluArgTrp.G
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                                                                         lAspSerPheGlyGlyLeuSerLysAlaProLysSerLeuProAlaLysS 83
                                                                                                                   SerThrSerProGlnSerGlnLeuAsnAspSerSerGluValLeuProVa
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                                                  .....TCGGGTGCGCCCTCAGTCCCAACCTCCCCGCCCTTGTCAT
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/note= "actual exon end not indicated in specification,
nucleotide indicated here is end of coding
sequence, TGA stop codon found at 2603-2605"
                                                                                                                                                                                                                        169.50
0.807
48.837
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                                                                                                                                                          from: 1
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Gaps: 24
Percent Identity: 23.953
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6
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2338	2289 CACTCGTAAGTCTTCCTTCCTGCCACTGGGATTCTTGAAACACCGTCTCAC
310	310 er
310 2288	299
298 2238	snSerG
287 2188	uGlySerI
271 2167	263 sLys
263 2118	248 ValIleGlyMetValGlyGlyTyrLeuAlaAspPheLeuLeuThrLy ::::: :::: 2069 CTGCTGGGGAATGCCATATTCGGCCAAGCCTCTGACCGGATTCTGTCCAA
247 2068	231 snIleArgAspAsnGlyLeuLeuSerAlaLeuProPheIleValAlaTrp ::::::::::::::::::::::::::::::::::::
231 2021	214 rThrmetValValTyrIleProThrTyrIleSerSerValTyrHisValA :::
21 4 1975	200TrpSerIleCysLeuGlyCysPheSerHisGlnTrpLeuValSe ::: :::
199 1930	189ProIleLysAlaMetLeuArgSerLeuProIle
1883	1834 TACCTCAGCACTAGCGGACACCTCGAGTCGACGCGCTCGGATTTCCCGGT
188 1833	IleIleSerSerLeuLysGlnGlnValGlySerSerLysGlnF
172 1795	159Pro.ValSerTyrProTrpIleSerThrSerGluLysGluTyr
158 1751	155 IleTyrAspAsp
154 1701	140PheGlyGlyValGlyCysValCysCysLeuLeuTrpPheValVal ::: :::
139 1651	123 eGlyGlyPheIleSerGluThrLeuGlyTrpProPheValPheTyrIle. : :::::: ::: ::: :::::
123 1601	107 SerileAlaLeuSerGlyMetLeuLeuGlyCysPheThrAlaIleLeuIl::::
106 1551	97 lyProProGlnGluArgSerArgLeuCys

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Claim 1; Page 1150-1151; 3271pp; English.

Chaim 2; Page 1150-1151; 3271pp; English.

Chaim 3; Page 1150-1151; 3271pp; English.

Chaim 3; Page 1150-1151; 3271pp; English.

Chaim 3; Page 1150-1151; 3271pp; English.

Chaim 4; Page 1150-1151; 3271pp; English.

Chaim 5; Page 1150-1151; 3271pp; English.

Chaim 5; Page 1150-1151; 2019; English.

Chaim 5; Page 1150-1151; 2019; English.

Chaim 5; Page 1150-1151; 2019; English.

Chaim 6; Page 1150-1151; 2019; English.

Chaim 6; Page 1150-1151; 2019; English.

Chaim 1; Page 1150-1151; 2019; English.

Chaim 6; Page 1150-1151; 2019; English.

Chaim 7; Page 1150-1151; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 2019; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block;
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07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-S.aureus vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
                                                  for recombinant production of the polypeptides. The new DNA sequences (and their fragments) are useful as primers or probes for isolating homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 97-374922/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6-MAR-1999 (first entry)
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           Staphylococcus aureus contig SEQ ID #112. Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                    V74423 standard;
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EP-786519-A2.
30-JUL-1997;
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ,
Rosen CA;
WPI; 97-374922/35.
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    Quality:
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Similarity:
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CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences confit the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so conduct that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are concerned in a vaccine composition against S.aureus infection of the used in a vaccine composition against S.aureus infection of collypeptides can also be used in a kit for the immunodetection of concerned sequences and surgical wound infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used computer readable medium.

CC computer readable medium. Sequence 18613 BP; Α, Ç 3477 9

45.663

138.50 0.774

Percent

Identity:

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Align seg 1/1 . 6 V74423 from: 6 18613

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213	197 9554	180 9509	170 9469	157 9419	144 9369	131 9319	116 9269	99 9246	94 196	84 9146
	LeuProIleTrpSerIleCysLeuGlyCysPheSerHisGlnTrpLeuVa 2	InvalGlySerSerLysGlnProLeuProIleLysAlaMetLeuArgSer 1	TTGGGAAGAGCCGGTCGATAAAGAAAATATTGATTCTCAA	AspAspProValSerTyrProTrpIleSerThrSerGlu 169	GlyCysValCysCysLeuLeuTrpPheValValIleTyr 1	uGlyTrpProPheValPheTyrIlePheGlyGlyVal	GlyCysPheThrAlaIleLeuIleGlyGlyPheIleSerGluThrLe		94	SerileLeuGlyGlyGlnPheAlaIleTrp
221	213 9576	196 9553	180 9508	169	156 9418	143 1368	131 9318	115 9268	99 9245	93 9195

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seq_documentation_block:
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                             30-OCT-1997; U19588.
31-OCT-1996; US-029960,
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon Kunsch CA, Rosen CA;
WPI; 98-272225/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer-readable medium with recorded Streptococcus pneumoniae
                                                                                                                                                                                                                                                                           Streptococcus pneumoniae genome fragment SEQ ID NO:32. Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay; computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                     WO9818931-A2.
                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 IleValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLe 302
                                                                                                                                                                                                                                                                                                                                                                                                                                  V52165 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNNCGCGTATCTATTCGGTGACTCAATGGCGAAAGTTGGTTTGGCGGCTA 10007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGTCTTATTC.....TACACAAATGCTACAAGTGT 9828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InGluTrpAlaLysGluArgLysLeu 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTATTCCTAGGCATG.....ATTCTATTAGGAATCGTTGCTTTCT 10133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..GGTGCGTTAATCTTTGGTCCGCAATTATTAATTGGTGTATCNNNNNNN 9907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hrValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeu 285
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alignment_block:
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                                                                                                                                                                                                                                                              9444 GTACAGTTTTCTTACTGGTTGGTAGTTTTCTATTTTTAGCTGCTATTTTG
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182 lySerSerLysGlnProLeuProIleLysAlaMetLeuArgSerLeuPro 198
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Claim 1; Page 326-332; 1409pp; English.
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                                                                                                                                                                                                                                                                                                                                                            ACTATTTGCTTTATCAAGGAAGATTTTCAACCAGTA........
                                                                                                                                                                                                                                                                                                         roPheValPheTyrIlePheGlyGlyValGlyCysValCysCysLeuLeu
                                                                                                                  eSerThrSerGluLysGluTyrIleIleSerSerLeuLysGlnGlnValG
                                                                                                                                                                                                             TrpPheValValIleTyrAspAsp.....ProValSerTyrProTrpIl 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgSerArgLeuCysSerIleAlaLeuSer...GlyMetLeuLeuGlyCy 117 ::::||| ::: |||
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Polynucleotide(s) and proteins derived stored on computer readable medium and anti-S.aureus vaccines
                                                                                                                                                                                                                             07-JAN-1997; 100117.
05-JAN-1996; US-009861
(HUMA-) HUMAN GENOME SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                            Rosen CA;
                                                                                                                                                                                                     Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus aureus
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                                                                                                                   WPI: 97-374922/35.
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                                                                                                                                                                                             SC, Choi GH, Dillon PJ,
                                                                                                                                                                                                 Fannon
                                                                                                                                                                                                     MR, Kunsch
                                from Staphylococcus aureus used in the production of
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seq_name: N_Geneseq_36:x07357
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US-09-391-958-1 x V74708
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Critis sequence represents one of 5191 Staphylococcus aureus DNA sequences CC of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using CC the S.aureus DNA sequences allows putative functions to be assigned so CC that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are CC likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The CC s.aureus in a sample. S.aureus is implicated in numerous human diseases, CC including cellulitis, eyelid infections, food poisoning, osteomyelitis, CC skin and surgical wound infections, scalded skin syndrome, toxic shock CC syndrome, etc. Organisms transformed with the DNA sequences can be used CC ind their fragments) are useful as primers or probes for isolating CC homologues of any of the S.aureus DNA sequences contained on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                               _documentation_block:
x07357 standard; DNA; 1386 BP
EP-893499-A2.
27-JAN-1999.
10-JUL-1998; 305495.
23-JUL-1997; US-898976.
                                                                                                                                                                                                                                          Staphylococcus aureus tetracycline resistance gene. Tetracycline resistance; antibiotic; antibacterial; screening; infection; otitis media; endocarditis; abscess; conjunctivitis;
                                                                                                                                                                                                                                                                                                       x07357;
21-MAY-1999 (first entry)
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                                                                                                                                           misc_feature
                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                        diagnosis;
                                                                                                                                                                                                                         epididymitis; toxic shock syndrome; sepsis; septic arthritis;
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Sequence 415 BP; 122 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGCATTTAACTGGCAAGCAGTATTTTACATTTTTGGTGCAGTAGGTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGWATGGTTAATGAAGCGGAGAAACGTTTCATTATGGAAAAT 398
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                                                                                                                                                                                                      therapy; vaccine;
                                                                                                                                                                                   aureus
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                                                                                        /note= "this nucleotide sequence is also disclosed
in the invention"
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64.198
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                                                                                                                                                              Location/Qualifiers
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Percent Identity:
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alignment_block: alignment_scores: cover or under expression of TR protein by identifying mutations in C the TR gene, or determining TR polypeptide or mRNA expression levels due to an infection of an organism with the TR gene (claimed). CC They can diagnose the stage and type of infection. TR polypeptides CC are also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for screening for compounds which affect the care also useful for careful candinistration of TR polypeptides can be used to treat conditions of associated with a lack of TR (claimed). Direct administration of CC antisense oligonuclectides prevents expression. TR polypeptides candinistration of candinistrated directly, in a vector (gene therapy) and as a vaccine) candination antibodies induce an immune response to immunise and prevent conclude: bacterial, especially S. aureus, infections of the careful decrease (claimed). Diseases diagnosed, prevented or treated conclude: bacterial, especially S. aureus, infections of the careful abscess), gastrointestine (e.g. splenic abscess), CNS (e.g. CC cerebral abscess), eve (e.g. conjunctivitis), kidney and urinary concludes induced and bone and joint (e.g. septic arthritis). TR polypeptides, polynucleotides and their (ant)agonists can prevent cathesis and body implants to prevent bacteria, infection Align seg 1/1 to: x07357 from: 1 US-09-391-958-1 x X07357 Percent Similarity: 391 362 AAACTGCC..... 312 TAACATTTTCCAACATCAATCCCCATTAACTTTAGTTGGACGTATTATTC 274 TATGGCGTGATATTAATCATT.....TTCGGATCAATTATTGG Claim 4; Page 25-27; 35pp; English.

Claim 4; Page 25-27; 35pp; English.

This is the coding region of a new Staphylococcus aureus gene encoding tetracycline resistance protein (see w97820) that is involved in sugar or drug transport across bacterial cytoplasmic membranes. The gene can be isolated from an S. aureus WCUH29 (NCIMB 40771) DNA library. Vectors comprisons the claimed 83 67 wounds and body implants to prevent bacterial infection. transcribed during both chronic and acute infections. (NCIMB 40771) DNA library. Vectors comprising the claimed polynucleotide, host cells and a process for producing the tetracycline resistance (TR) protein are claimed. TR polypeptides and polynucleotides are useful for diagnosing diseases related to 50 erThrSerProGlnSerGlnLeuAsnAspSerSerGluValLeuProVal 66 Sequence 36 nAsnValIleMetAsn.....IleThrMetValAlaMetValAsnS 50 20 TyrGlyIleAlaLeuValLeuHisPheCysAsnPheThrThrIleAlaGl 36 New Staphylococcus aureus tetracycline resistant protein and gene useful as diagnostic reagents and for prevention and treatment of staphylococcal infections, including toxic shock syndrome and otitis (SMIK) SMITHKLINE BEECHAM CORP.
(SMIK) SMITHKLINE BEECHAM PLC.
Burnham MKR, Lonetto MA, Warren PV; P-PSDB; W97820 rSerIleLeuGlyGlyGlnPheAlaIleTrp...GluArgTrpGlyProP 99 AspSerPheGlyGlyLeuSerLysAlaProLysSerLeuProAlaLysSe 83 Quality: Ratio: 122.50 0.583 47.945 ВP; ...TTATATGTGATATATGTTGCAAAGTATCTTTCTA 424 414 A; Percent Identity: 18 for diagnosing diseases related to to: 1386 212 C; Length: Gaps: <u>ი</u> 390 369 311 TR is

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347	.laSerArgGlyPheSerSerIleAlaProValIleV	ω
330 1212	14 GINSETGLYILGTYTILGASHVALLGUASPILGALBFROATGTYTSGETSG 15::::::::::::::: 16:::: 17:::::::::::::::::::::::::::::::	11
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97	ProTyrLeuAsnSerGlyTyrI	
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	33 ArgAspAspClvLouLeuscerhleIouDroDboTlowslalamansusli	.
232 900	16 etValValTyrIleProThrTyrIleSerSerValTyrHisValAsnIle ::: ::::::::::::::::::::::::::::::::	& N
216 850	99 eTrpSerIleCysLeuGlyCysPheSerHisGlnTrpLeuValSerThrm	8 1
199 800	83 SerSerLysGlnProLeuProIleLysAlaMetLeuArgSerLeuProIl 	7 1
182 750	1/2 y1.1=11=5=15=11euysGlnGlnValGly ::: ::: 701 ATATGATTGGTGCCTTAATTGCAATTATCGTTTTTGCGCTATATATTAAA	7
0 7	55 GTYTASPASPPTOVALSETTYPTOTTPILESETTHTSETGLULYSGLU 75 GTTTATTACGAACTTTAATTGGTTA	
155 674	0PheGlyGlyValo	
624	5 TCTTATTTAAATTATTACCAAAAGAAAATA	
139	35 heValPheTyrIle	
135 574	132 yTrpProp	
132 524	116 GlyCysPheThrAlaIleLeuIleGlyGlyPheIleSerGluThrLeuGl:::	
115 474	99 roglogluArgSerArgLeuCysSerIleAlaLeuSerglyMetLeuLeu :::::::::::::::::::::::::::::::::	

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154.52 154.52 .50 154

52 0.3864 52 0.3864 154.52 0.3

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Sequence | Service | Strid Orig | 2 Score | Escore | Len | Documentation | Documentation | Cogn2_6/prodata//Ina/Sc_COMB.seq:US-08-724-394A-19 + 2066.00 4273.05 | 1.5e-230 | 1843 | 1.5e-45 | 1.5e-230 | 1843 | 1.5e-230 | 1843 | 1.5e-230 | 1843 | 1.5e-45 | 1.5e-230 | 1843 | 1.5e-45 | 1.5e-230 | 1843 | 1.5e-45 | 1.5e-230 | 1.5e-230 | 1.5e-45 | 1.5e-2
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Database sequences: 230463
Database length: 64992525
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Query: US-09-391-958-1
Query length: 401
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-DB-ISSued_Patents_NA -QFMT-fastap -SUFFIX-rn1 -GAPOP=12.000
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-QGAPOP-4.500 -QGAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500
-FGAPOP-6.000 -FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.130000
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/cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-485-910-182 + 1
/cgn2_6/ptodata/1/ina/FUS_COMB.seq:PCT-US95-06566-156
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-466-033-234 + 1
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LIBRARY: BRAIT
CLONE: 754412
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leAlaGlnAsnValIleMetAsnIleThrMetValAlaMetValAsnSer
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alignment_block:
US-09-391-958-1 x US-08-805-118-2
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                                                                                                                                                                                                                                   Ratio: 5.177
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEED VERTSION 2.0
CURRENT APPLICATION DATA:
235 ATGCAAGTGGATGAGACACTGATCCCCAGGAAAGTTCCAAGTTTATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 POR CITY: Palo Alto STATE: CA COUNTRY: US
                                                                                                          1 MetGlnValAspGluThrLeuIleProArgLysValProSerLeuCysSe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/ina/5D_COMB.seq:US-08-805-118-2
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5, 5985604
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3174 Porter Drive
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Percent Identity:
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104.50
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                                                                                 lyAlaSerArgGlyPheSerSerIleAlaProVallleValProThrVal
                                                                                                                                                                              ulleThrValArgLySileAlaThrileLeuGlySerLeuProSerSerA 284
                                                                                                                                                                                                                                                                            SPASNGlyLeuLeuSerAlaLeuProPheIleValAlaTrpValIleGly 250
                                   TTATATCAATGTCTTAGATATTGCTCCAAGGTATTCCAGTTTTCTCATGG
                                                  eTyrIleAsnValLeuAspIleAlaProArgTyrSerSerPheLeuMetG
                                                                                                                                                                                                                             CACTCATTGTGTCTCTGCCTTACCTCAATTCCGGCTATATCACAGCAACT
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                                                                                                                                                                                                                                                                                                                                                                                     SerIleCysLeuGlyCysPheSerHisGlnTrpLeuValSerThrMetVa
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US-08-724-394A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5
                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/724
ETLING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                  STRANDEDNESS:
TOPOLOGY: not
MOLECULE TYPE: (
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION DATA:
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ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1235 GAGCATCAAGAGGATTTTCGAGCATAGCACCTGTCATTGTACCCACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Megabase Transcript Map: TITLE OF INVENTION: Sequences and Antibodies NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 heGlyGluAlaAspValGlnGluTrpAlaLysGluArgLysLeuThrArg 400
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            LOCATION: 1..1780 OTHER INFORMATION:
                                               NAME/KEY: misc_feature
                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                    not relevant
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                                                                                                                       not relevant
              /note=
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            "CDNA
                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
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alignment_scores:

Quality: 2061.00

Length:

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Align seg 1/1 to: US-08-724-394A-19
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                           1127
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                                                                          TrpPheValValIleTyrAspAspProValSerTyrProTrpIleSerTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GluargSerArgLeuCysSerIleAlaLeuSerGlyMetLeuLeuGlyCy 117
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uIleThrValArgLysIleAlaThrIleLeuGlySerLeuProSerSerA
                                       MetValGlyGlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLe
                                                                                                                                                                              CTAAGCAGCCTCTTCCCATCAAAGCTATGCTCAGATCTCTACCCATTTGG
                                                                                                                                                                                                                                              erLysGlnProLeuProIleLysAlaMetLeuArgSerLeuProIleTrp
                                                                                                                                                                                                                                                                                                   rSerGluLysGluTyrIleIleSerSerLeuLysGlnGlnValGlySerS 184
                                                                                                                                                                                                                                                                                                                                                                                                          roPheValPheTyrIlePheGlyGlyValGlyCysValCysCysLeuLeu 150
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                                                                                                                                                                                                                                                                                     CTCAGAAAAAGAATACATCATATCCTCCTTGAAACAACAGGTCGGGTCTT
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99.501
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Sequence 18, Application US/08724394A
Patent No. 587237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Ruddy, David A.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Toomas, Winston
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 587223
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO Embarcadero Center, 8th Floor
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ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION UNMBER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
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                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 heGlyGluAlaAspValGlnGluTrpAlaLySGluArgLySLeuThrArg 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 lyAlaSerArgGlyPheSerSerIleAlaProVallleValProThrVal 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                                                                                                                                                              SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                              STREET: Two Embarcade
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 laLeuIleValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThr
                                                                                                                    APPLICATION NUMBER: US/01
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||
TTA 1579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACTCATTGTGTCTCTGCCTTACCTCAATTCCGGCTATATCACAGCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ePheLeuLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIleP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerGlyPheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGCATCAAGAGGATTTTCGAGCATAGCACCTGTCATTGTACCCACTGTC 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTCTTGCTGTTTGCCGTTAACCTGTTAGGACTACTCTTCTACCTCATAT 1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leu 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGCGGATTTCTTAGTCAGGACCCTGAGTTTGGGTGGAGGAATGTCTT 1476
                                                                                                                                                               US/08/724,394A
                                                                                                                                                                                                Release #1.0, Version
                                             017957-000100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1376
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18:

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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc_feature
; LOCATION: 1..2266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2266 base pair
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                                                                                                                                                                                                                                            790
                                                                                                                                                                                                                                                                                               740 CCAAGTGGATATTTAGCAGGGATATTTGGAGCAAAAAAATGCTTGGTGC 789
                                                                                                                                                                                                                                                                                                                                                        690 AGGGTATCATCTTTAGCTCCATCAACTATGGGATAATACTGACTCTGATC 739
                                                                                                                                                                                                                                                                                                                                                                                                                 |||:::::: :::|||:::||:::||640 CAAGGAATTTGATACAAAGGCCTCTGTGTATCAATGGAGCCCCAGAAACTC 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          590 TCCACTGAGGGGCCTGTTGCAGATGCCTTCAATAACTCCAGCATATCCAT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 oProGlnGluArgSerArgLeuCysSerIleAlaLeuSerGlyMetLeuL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                            76 OLYSSerLeuProAlaLysSerSerIle..... 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
                          euGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSerGluThrLeu 131
                                                         TCCACTTGAACGAAGCAAGCTCACCACCATTGCAGGATCAGGGTCAGCAT
                                                                                                                                                                                                                                    TGGTTTGCTGATCTTCCCTTCTCACCCTCTTTACACCACTGGCTGCTG 839
                                                                                                                                                                                                                                                                  85
                                                                                                                                                                                                                                                                                                                           .....LeuGly.. 87
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3.305
59.873
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Gaps: 4
Percent Identity: 41.826
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 1039
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	148 1090	sLeuLeuTrpPheValValIleTyrAspAspProValSerTyrProTrpI 1	165 1139
	165 1140	leSerThrSerGluLysGluTyrIleIleSerSerLeuLysGlnGlnVal 1	181
	182 1190		198 1239
	198 1240	OlleTrpSerTleCysLeuGlyCysPheSerHisGlnTrpLeuValSerT 2 ::: :::	215 1289
c	215 1290	hrMetValValTyrIleProThrTyrIleSerSerValTyrHisValAsn 2 ::::::::: :::	231 1339
	232 1340	IleArgAspAsnGlyLeuLeuSerAlaLeuProPheIleValAlaTrpVa 24	248 1389
	248 1390	lileGlyMetValGlyGlyTyrLeuAlaAspPheLeuLeuThrLysLys. 2 :::::: ::::::: CTGTACAATTTTAGGAGGTCAGCTGGCAGATTTCCTTTTGTCCAGGAATC 1	264 1439
	265 1440	PheArgLeuIleThrValArgLysIleAlaThrIleLeuGlySerLeu 2 :::	280 1482
	281	ProSerSerAlaLeuIleValSerLeuProTyrLeuAsnSerGlyTyrIl 2	297
	1482		1482
	297	eThrAlaThrAlaLeuLeuThrLeuSerCysGlyLeuSerThrLeuCysG 3	314
	1482 314	lnSerGlyIleTyrIleAsnValLeuAspIleAlaProArgTyrSerSer 3	1482 330
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	331 1492	PheLeumetGlyAlaSerArgGlyPheSerSerIleAlaProValIleVa 34	47
	347 1542	ProThrValSerGlyPheLeuLeuSerGlnAspProGluPheGlyTrpA 36 	64 591
	36 4 1592	rgAsnValPhePheLeuLeuPheAlaValAsnLeuLeuGlyLeuLeuPhe 380 	380 16 4 1
	381 1642	TyrLeuilePheGlyGluAlaAspValGlnGluTrpAlaLysGluArgLy 397 ACCTCACGTTTGGACAAGCAGAACTTCAAGACTGGGCCAAAGAGAGAG	97
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; Patent No. 5618677

seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-647-484-1

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	1030	1030
	78	62 GluValLeuProValAspSerPheGlyGlyLeuSerLysAlaProLysSe
	1030	1023 CCGCCTGC
	61	45 alAlaMetValAsnSerThrSerProGlnSerGlnLeuAsnAspSerSer
	45 1022	28 eCysAsnPheThrThrIleAlaGlnAsnValIleMetAsnIleThrMetV
	28 979	12 VALFOSETLEUCYSSETALARIGTYGTYLLEALALEUVALLEUHISPN ::: ::: ::::: 941 ATCCCCTCAGCTGCCCGCGTCCACTATGGCTGTGTCATC
	3	eg 1/1 to: US-08-647-484-1 from: 1 to: 2716
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		ICE ADDRESS Lilly Corpolianapolis United Sta IS Floppy IBM PC CO SYSTEM: PC CO FATION DATA ATION UNMBER: TION LATA UNUMBER: TONCKET NUM ATION INFORMA LON REQ ID RECTERISTII UNITED STA UNI
IC ACID COMPOUNDS	SANIC ED NUCLEIC	GENERAL INFORMATION: APPLICANT: NI, Binhui APPLICANT: Paul, Steven M. TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NU NUMBER OF SEQUENCES: 3

CAACGGCGTGGGCACACTGTCGGGCATGGTGTGCCCCATCATCGTGGG heLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheL :::
82 CCAACGGCGTGGGCACACTGTCGGGCATGGTGTGCCCCATCATCGTGGGG 18
36 erArgGlyPheSerSerIleAlaProValIleValProThrValSerGly 35
319 eASNVALLEUASPIleAlaProArgTyrSerSerPheLeuMetGlyAlaS 336 :
303 LeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrIl 319
286 leValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeu 302 ::::: ::::: :::::: ::::::
270 .ValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeuI 286
254 GlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeuIleThr 269
237 euLeuSerAlaLeuProPheIleValAlaTrpValIleGlyMetValGly 253 :::
220 eProThrTyrIleSerSerValTyrHisValAsnIleArgAspAsnGlyL 237 ::::::: :::
204 LeuGlyCysPheSerHisGlnTrpLeuValSerThrMetValValTyrIl 220 :::::: :::::: ::::::: ::::::
189ProIleLysalaMetLeuArgSerLeuProIleTrpSerIleCys 203
178 sGlnGlnValGlySerSerLysGlnProLeu
· tó
145 ysValCysCysLeuLeuTrpPheValValIleTyrAspAspProValSer 161 ::: ::: ::::: ::: 1197 TCTTCTGGTACCTGTTCTGGCTCGTCTCCTACGAGTCCCCCGCGCTG 1246
128 rGluThrLeuGlyTrpProPheValPheTyrIlePheGlyGlyValGlyC 145
112 GlyMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSe 128
95 rgTrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 111

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US-09-391-958-1 x US-08-647-484-3
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Quality:
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US-08-647-484-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
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                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-647-484-3 from: 1 to: 2716
                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/647,484
FILING DATE: 14-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,033
FILING DATE: 27-APR-1995
ATTORNEY/ACENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10006
TELEPHONE: (317) 276-0756
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08647484 Patent No. 5618677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (317) 276-
TELEFAX: (317) 276-38
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
1023 CCGCCUGC...... 1030
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                                                                                             980 ......UUCGUGAGGAUCCUGCAGGGGUUGGUAGAGGGGGGUCACAUACC 1022
                                                                                                                                                                                     941 AUCCCCUCAGCUGCCCGCGUCCACUAUGGCUGUGUCAUC...... 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2716 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ni, Binhui
APPLICANT: Paul, Steven M.
APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 luAlaAspValGlnGluTrpAlaLysGluArgLysLeuThr 399
                                                                                                                                         28 eCysAsnPheThrThrIleAlaGlnAsnValIleMetAsnIleThrMetV 45
                                                 45 alAlaMetValAsnSerThrSerProGlnSerGlnLeuAsnAspSerSer 61
                                                                                                                                                                                                                        12 ValProSerLeuCysSerAlaArgTyrGlyIleAlaLeuValLeuHisPh ::::|||||| :::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Lilly Corpo
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States of America
                                                                                                                                                                                                                                                                                                                                                                                                           479.00
2.056
58.690
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, 276-3861
, 200: 3:
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 7
Percent Identity: 28.212
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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62	GluValLeuProValAspSerPheGlyGlyLeuSerLysAlaProLysSe 7	8
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1031	GAUCUGGAG)46
95 1047	rgTrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 11 :: :::)96
112 1097	GlyMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSe 12 ::: ::: ::: 	86
128	luThrLeuGlyTr ::	'n
1147	AUGGAGCUCUGUUUUCUACGUCUACGGCAGCUUCGG	.96
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162 1247	TyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLy 17 ::: ::: :::: caccccagcaUcUcGgaggaggagcgcaaguacaUc	84
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270 1585	.ValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeuI 28 ::: :: CGUGCGCAAGUUGAACUGCGGAGGCUUCGGCAUGGAAGCCACGCUGC 16	34
286 1635	leValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeu 30 :::::	81
303 1682	LeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrIl 31 ::: ::: ::: ::::: ::: :: CUGGUCCUAGCCGUGGGCUUCAGCGGCUUCGCCAUCUCUGGGUUCAACGU 17	31
319 1732	eAsnValLeuAspIleAlaProArgTyrSerSerPheLeuMetGlyAlas 33:	81
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Quality:
Ratio:
Percent Similarity:
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US-08-647-481-1
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US-09-391-958-1 x US-08-647-481-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/430,033
APPLICATION NUMBER: US 08/430,033
APPLICATION NUMBER: 27-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: N1, BINNLI
APPLICANT: N1, STAVEN M.
APPLICANT: PAUL Steven M.
APPLICANT: PAUL STEVEN M.
APPLICANT: PAUL STEVEN M.
APPLICANT: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1882 UGCCUCCCUGGUGCACUAUGGAGGUGUCAUCUUCUACGGGGUCUUUGCUU 1931
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OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,481
FILING DATE: 14-MAY-1996
CIACITETE TO TO THE STATEMENT APPLICATION THE STATEMENT APPLICATION TO THE STATEMENT APPLICATION TO THE STATEMENT APPLICATION TO THE STATEMENT APPLICATION TO THE STATEMENT 
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     386 luAlaAspValGlnGluTrpAlaLysGluArgLysLeuThr 399
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 uLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyG 386
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12 ValProSerLeuCysSerAlaArgTyrGlyIleAlaLeuValLeuHisPn 28
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2.056
58.690
                                                                                                                                                                                                                                                                                                                           Length: 397
Gaps: 7
Percent Identity: 28.212
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270 .ValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeuI 286
4 GlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeuIleThr
7 euLeuSerAlaLeuProPheIleValAlaTrpValIleGlyMetValGly ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
eProThrTyrIleSerSerValTyrHisValAsnIleArgAspAsnGlyL
LeuGlyCysPheSerHisGlnTrpLeuValSerThrMetValValTyrI1 ::::: ::::: ::::: ::::: ::::: ::::: ::::::
ProlleLysAlaMetLeuArgSerLeuProlleTrpSerIleCys
SGInGInValGlySerSerLySGInProLeu ::::::::::::::::::::::::::::::
TyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLy 178 :::
ysValCysCysLeuLeuTrpPheValValIleTyrAspAspProValSer 161 TCTTCTGGTACCTGTTCTGGCTGCTCGTCTCTACGAGTCCCCCGGCTG 124 TyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLy 178 :::
rGluThrLeuGlyTrpProPheValPheTyrllePheGlyGlyValGlyC 145 :::
GlyMetLeuLeuGlyCysPheThralaIleLeuIleGlyGlyPheIleSe 128
rgTrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 111 ::: ::
LIGUPTOALALYSSETSETILEIGUGLYGIYGINPHALAILTETGAILAPS
rLeuProAlaLysSerSerIleLeuGlyGlyGlnPheAlaIleTrpGluA 95
GluvalLeuProvalAspSerPheGlyGlyLeuSerLysAlaProLysSe 78 **CeuProAlaLysSerSerIleLeuGlyGlyGlnPheAlaIleTrpGluA 95 **IFEUProAlaLysSerSerIleLeuGlyGlyGlnPheAlaIleTrpGluA 95 **IFTPGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 111 **IFTPGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 111 **ATGGGCCCCCCTTTGGAAGGGATGCCCCTGGCAGCACACCTTTTGT 109 GlyMetLeuLeuGlyCysPheThrAlaIlLeulleGlyGlyPheIleSe 128 GTTCCTATGCTGGGCGGTGGTGGCCGTGGCCGCGCGCGCG

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; MOLECULE TYPE: mRNA
US-08-647-481-3
                                                                      alignment_scores:
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Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/430,033

FILING DATE: 27-APR-195

ATTORNEY/AGRENT IMPORMATION:

NAME: Gaylo, Paul J.

REGISTRATION NUMBER: 36,808

REFERENCE/DOCKET NUMBER: X-10006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 276-0756
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APPLICANT: Ni, Binhui
APPLICANT: Ni, Binhui
APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                             TELEFAX: (317) 276-3861 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2716 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
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                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-MAY-1996
CLASSIFICATION: 536
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  Percent Identity: 28.212
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                   Gaps:
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alignment_block:
US-09-391-958-1 x US-08-647-481-3
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1585 CGUGCGCAAGUUGAUGAACUGCGGAGGCUUCGGCAUGGAAGCCACGCUGC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1385 GUGGCCAACUUCUGCCGCAGCUGGACGUUCUACCUGCUGCUCAUCUCCCA 1434
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                                                    270 .ValArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeuI 286
                                                                                                                                              254 GlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeuIleThr..
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                                                                                                              GGCCAGAUCGCGGACUUCCUGCGGAGCCGCCGCAUCAUGUCCACCACCAA 158
                                                                                                                                                                                                                            UGGUGUCCGCGCUGCCCACCUGGUCAUGACCAUCAUCGUGCCCAUCGGC
                                                                                                                                                                                                                                                                                                                                        GCCCGACUACUUCGAAGAAGUGUUCGGCUUCGAGAUCAGCAAGGUAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UCUUCUGGUACCUGUUCUGGCUGCUCGUCCUACGAGUCCCCCGCGCUG 1246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGUACUCAGGAUGGAGCUCUGUUUUCUACGUCUACGGCAGCUUCGGGA 1196
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08430033A Patent No. 5686266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                     TELEFAX: (317) 276-3861 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1732 GAACCACCUGGACAUAGCCCCGCGCUACGCCAGCAUCCUCAUGGGCAUCU
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                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: N1, Binhui
APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
NUMBER OF SEQUENCES: 3
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2716 base pair
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: X-10006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 luAlaAspValGlnGluTrpAlaLysGluArgLysLeuThr 399
                                                         FEATURE:
                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                NAME/KEY:
                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
         LOCATION:
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                                                                                                                                                nucleic acid
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                                                                                                                                                                      2716 base pairs
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CDS
461..2140
                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                          36,808
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alignment_block:
US-09-391-958-1 x US-08-430-033A-1
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 GlyMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSe 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ValProSerLeuCysSerAlaArgTyrGlyIleAlaLeuValLeuHisPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysValCysCysLeuTrpPheValValIleTyrAspAspProValSer 161
                                                euLeuSerAlaLeuProPheIleValAlaTrpValIleGlyMetValGly 253
                                                                                                                                                                                                                                                                                                                                                                                        GACGCCATCGGAGAGAGCGCGAAACTCATGAACCCCCTCACGAAGTTTA 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                 sGlnGlnValGlySerSerLysGln......ProLeu...... 188
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TGGTGTCCGCGCTGCCCCACCTGGTCATGACCATCATCGTGCCCCATCGGC 1534
                                                                                                GCCCGACTACTTCGAAGAAGTGTTCGGCTTCGAGATCAGCAAGGTAGGCC 1484
                                                                                                                                           eProThrTyrIleSerSerValTyrHisValAsnIleArgAspAsnGlyL 237
                                                                                                                                                                                            GTGGCCAACTTCTGCCGCAGCTGGACGTTCTACCTGCTGCTCATCTCCCA 1434
                                                                                                                                                                                                                                          LeuGlyCysPheSerHisGlnTrpLeuValSerThrMetValValTyrIl 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCTGGTACCTGTTCTGGCTGCTCGTCTCCTACGAGTCCCCCGCGCTG 1246
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2.056
58.690
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seq_documentation_block:
; Sequence 3, Application
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                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEPHONE: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quence 3, Application US/08430033A tent No. 5686266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1832
                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,033A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2716 base pair
                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1635 TGTTGGTCGGCTACTCGCACTCCAAGGGCGTG...GCCATCTCCTTC 1681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ni, Binhui
APPLICANT: Paul, Steven M.
APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPORTER AND RELATED NUCLEIC ACID COMPOUNDS
CORRESPONDENCE ADDRES: 3
CORRESPONDENCE ADDRES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 PheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLe 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286 leValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeu 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Lilly Corpo
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCATGACTAAGCACAAGACTCGGGAGGAGTGGCAGTACGTGTTCCTAAT 1881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyG 386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Eli Lilly and Company
Lilly Corporate Center
2716 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
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;; ; US-08-	TYPE: nucleic acid STRANDEDNESS: single TOPOLCGY: linear MOLECULE TYPE: mRNA 18-430-033A-3
alignment Percent	ent_scores: Quality: 479.00 Ratio: 2.056 nt Similarity: 58.690 Percent Identity: 28.212
alignment_b US-09-391-	lock: 958-1 x US-08-430-033A-3
Align	seg 1/1 to: US-08-430-033A-3 from: 1 to: 2716
9 .	12 ValProSerLeuCysSerAlaArgTyrGlyIleAlaLeuValLeuHisph 28 ::: ::: ::::: :::::: 979
9	Ile :::
	45 alAlaMetValAsnSerThrSerProGlnSerGlnLeuAsnAspSerSer 61
. 10:	
1030	
78	rLeuProAlaIlysSerSerIleLeuGlyGlyGlnPheAlaIleTrpGluA
10	95 rgTrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 111
1047	17 AAUGGGCCCACCCUUAGAACGGAGUCGCCUGGCGACGACAGCCUUUUGU 1096
112 1097	12 GlyMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSe 128
128 1147	28 rGluThrLeuGlyTrpProPheValPheTyrIlePheGlyGlyValGlyC 145 ::: ::::: ::: 17 GCAGUACUCAGGAUGGAUCUGUUUUCUACGUCUACGCAGCUUCGGGA 1196
145 1197	S ysValCysCysLeuLeuTrpPheValValIleTyrAspAspProValSer 161
162 12 4 7	72 TyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLy 178 ::: ::: ::: :: CACCCCAGCAUCUCGGAGGAGCGCGAAGUACAUC
178 1285	8 sGlnGlnValGlySerSerLysGlnProLeu 188 :::: ::: ::: :::
18 133	5 9
20 138	04 LeuGlyCysPheSerHisGlnTrpLeuValSerThrMetValValTyrI1 220 :::::: ::::::::::::::::::::::::
220 1435	0 eProThrTyrIleSerSerValTyrHisValAsnIleArgAspAsnGlyL 237

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seq_documentation_block:
; Sequence 1, Application PC/TUS9605792
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                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: API11 27, 1
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPROTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ni, Binhui APPLICANT: Paul, Stev
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                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Lilly Corpo
CITY: Indianapolis
STATE: Indiana
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X:
                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US96/05792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLe
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                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                     Paul J.
                                                                                                                    08/430,033
  x-10006
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alignment_block:
US-09-391-958-1 x PCT-US96-05792-1
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TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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1335 GCACTCCTGGCGGCGCTTCTTCACGTCTATGCCAGTCTATGCCATCATC 1384
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                               145
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                                                                                                                                                                            CACCCCAGCATCTCGGAGGAGGAGCGCAAGTACATC......GA 1284
                                                                                                                                                                                                                   TyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLy 178
                                                                                                                                                                                                                                                                                                                                                        GCAGTACTCAGGATGGAGCTCTGTTTTCTACGTCTACGGCAGCTTCGGGA 1196
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                                                                                                                                                                                                                                                                                                          ysValCysCysLeuTrpPheValValIleTyrAspAspProValSer 161
                                                                                                                                                                                                                                                                                                                                                                               rGluThrLeuGlyTrpProPheValPheTyrIlePheGlyGlyValGlyC 145
                                                                                                                              sGlnGlnValGlySerSerLysGln......ProLeu...... 188
                                       .....ProIleLysAlaMetLeuArgSerLeuProIleTrpSerIleCys 203
                                                                                       GGACGCCATCGGAGAGAGCGCGAAACTCATGAACCCCCTCACGAAGTTTA 1334
                                                                                                                                                                                                                                                                   TCTTCTGGTACCTGTTCTGGCTGCTCGTCTCCTACGAGTCCCCCGCGCTG 1246
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461..2143
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2.056
58.690
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Percent Identity: 28.212
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application
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                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1385 GTGGCCAACTTCTGCCGCAGCTGGACGTTCTACCTGCTGCTCATCTCCCA 1434
                                                                                                                                                                                                                                                                                                                         APPLICANT: N1, Binhui
APPLICANT: Paul, Steven M.
TITLE OF INVENTION: HUMAN BRAIN SODIUM DEPENDENT INORGANIC
TITLE OF INVENTION: PHOSPHATE COTRANSPROTER
NUMBER OF SEQUENCES: 3
                        CURRENT APPLICATION DATA:
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 luAlaAspValGlnGluTrpAlaLysGluArgLysLeuThr 399
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                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                         COUNTRY:
  APPLICATION NUMBER:
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                                                                                                                                                                     46285
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                                                                                                                                                                                      United States of America
PCT/US96/05792
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alignment_block:
US-09-391-958-1 x PCT-US96-05792-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: PCT-US96-05792-3 from: 1
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1031
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                                     1247 CACCCCAGCAUCUCGGAGGAGGAGCGCAAGUACAUC.....GA
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                                                                                162 TyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerLeuLy 178
                                                                                                                                                                                                                                      112 GlyMetLeuLeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSe 128
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LENGTH: 2716 base pairs
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FILING DATE: April 27, 1
ATTORNEY/AGENT INFORMATION:
178 sGlnGlnValGlySerSerLysGln......ProLeu......
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                          ysValCysCysLeuTeuTrpPheValValIleTyrAspAspProValSer 161
                                                                                                                                                                                                             GCAGUACUCAGGAUGGAGCUCUGUUUUCUACGUCUACGGCAGCUUCGGGA 1196
                                                                                                                                                                                                                                                                                                                                                                                                             rgTrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSer 111 ::!||::: |||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....CAUGGGAUCUGGAGCA 1046
                                                                                                                          UCUUCUGGUACCUGUUCUGGCUGCUCGUCUCCUACGAGUCCCCCGCGCUG 1246
                                                                                                                                                                                                                                                                                                    GluValLeuProValAspSerPheGlyGlyLeuSerLysAlaProLysSe 78
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Percent Identity:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08805118 Patent No. 5985604
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1385
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                                                                                                                                                     APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
TITLE OF INVENTION: PHOSPHATE CO-TRANSPORTER
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 luAlaAspValGlnGluTrpAlaLysGluArgLysLeuThr 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            353 PheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLe 369
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                                                                                                                                                CORRESPONDENCE ADDRESS:
COUNTRY: US
ZIP: 94304
                                                                             STREET:
                                                      STATE:
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUGGCCAACUUCUGCCGCAGCUGGACGUUCUACCUGCUGCUCAUCUCCCA 1434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyTyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeuIleThr.. 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCACUCCCUGGCGCGCUUCUUCACGUCUAUGCCAGUCUAUGCCAUCAUC 1384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUGGAGAGAAGCAGCCGUGGGCAGAGCCUGAGGAGAUGAGC 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAACGGCGUGGGCACACUGUCGGGCAUGGUGUGCCCCAUCAUCGUGGGG 1831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUGGUCCUAGCCGUGGGCUUCAGCGGCUUCGCCAUCUCUGGGUUCAACGU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGUGCGCAAGUUGAUGAACUGCGGAGGCUUCGGCAUGGAAGCCACGCUGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrIl 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCCAGAUCGCGGACUUCCUGCGGAGCCGCCGCAUCAUGUCCACCACCAA 1584
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                                                                          Palo Alto
                                           CA
                                                                                                 E: Incyte Pharmaceuticals, 3174 Porter Drive
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; LIBRARY: BRAT; ; CLONE: 754412
US-08-805-118-5
seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-391-958-1 x US-08-805-118-5
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                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-055
TELEPAX: 415-845-4177
                                                                                                                                                                                                                     333 tGlyAlaSerArgGlyPheSerSerIleAlaProValIleValProThrV 350
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LENGTH: 272 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                          151
                                                                                                                                                                                                                                                                                                                                                                   317 IleTyrIleAsnValLeuAspIleAlaProArgTyrSerSerPheLeuMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                              400
                                                                                                                                                                                        367 PhePheLeuLeuPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIl 383
                               251 GTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                      51 GGGAGCATCAAGAGGATTTTCGAGCATAGCACCTGTCATTGTACCCACTG
                                                                                                                                                                                                                                                                                                                                                    1 ATTTATATCAATGTCTTAGATATTGCTCCAAGGTATTCCAGTTTTCTCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/8 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 2.0
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Gaps:
Percent Identity:
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seq_documentation_block:

Sequence 20, Application US/08724394A Patent No. 5872237

GENERAL INFORMATION:
APPLICANT: Feder,
APPLICANT: Kronma

Feder, John N. Kronmal, Gregory S.

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alignment_block:
US-09-391-958-1 x US-08-724-394A-20/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-08-724-394A-20 from: 1
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
DEFENDENCE TOTOGET NUMBER: 017057-000100
                                                             22180 CCTTGTACCTGTGGCCCATGCAGAGGTCTCTAGGGCAGGGTGTGGATCTC 22131
                                                                                                                                                                                                                                               22230 GGGAAAAGGAGCACATCCTGTCCTCACTGGCTCAACAGGTACAGTGCACA 22181
                                                                                                                                                                                                                                                                                                                                      22330 TTTTATCCCTTCTTCCCAGGTAGCACTGGCTGTGTCTGCTGTCTCCTATG 22281
                                                                                                                                                                               168 erGluLysGluTyrIleIleSerSerLeuLysGlnGlnValGly..... 182
                                                                                                                                                                                                                                                                                                                                                                  137 PheTyrIlePhe.....GlyGlyValGlyCysValCysCysLeuLeuTr 151
183 rSerLysGln..Pro.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94111-3834
                                                                                                         ......se 183
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Ruddy, David A.
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1.848
29.650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 543
Gaps: 10
Percent Identity: 20.994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       017957-000100
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                     187
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A 21231	21280 CCCAGAGTGATGCAGCTTCTGGCCCCTCTTATCTGAGACAGTGTTCTTTTA	
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G 21281	21330 CCGTTTCAAAAACAAAAAACCCAAGAAATTAATATTGCTTTTATCTGGAG	
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т 21331	21380 TGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGCGACAGAGTAAGACT	
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T 21381	21430 AGGAGGCTGAGACAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAT	
. 234	234	
C 21431	21480 TACAAAAATTAGCCAGGTGTGGTGGCAGGCACCTGTAATCCCAGCTATTC	
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A 21531	21580 TAATTCCAGCACTTTGGGAGGCCGAGGCAGGCAGATCATGAGGTCAGGAA	
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. 234	234	
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;G 21781	21830 GGCTTTACATATAACCATTAATTTAACCTTCACAATGACCTTGAGAGAGG	
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T 21831	21880 AATGATAATGGTAATAAGGAGAAACAGTTCTGTGTTACCTATTACATTCT	
. 234	234	
234 AA 21881	22/ 1TyTH15ValAsnIleArgAsp	
ln 210 rc 21981	194 eUATGSerLeubrolleTipSerlleCysLeuGlyCysPheSerHisGln ::	
G 22031	TTCT	
LL 194	188LeuProIleLysAlaMetL	
CT 22081	22130 CTCTGAGAGGCACCATCTTGGCTGCTCTAATACTCATGCTGATTAGATCT	

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seq_documentation_block:
; Sequence 21, Application US/08724394A
; Patent No. 5872237
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COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20780 GACCAGTAACCTATGTGACTCAGGGTTTATCATCAACACCTTAGATATCG 20731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20880 ATTGCCCAGGGCTCCTTCCATCAATATGTGCTGTGGCCCTGCCCTTT 20831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20930 AATCCCTTTTCTGCACATGGTCTCAGAGGGTTCCCTGACAGCATGTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20980 AAAGCTCTTTTCATCTTTGGTAAGGATAAGCGTGTGGGCCCATTTAACC 20931
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map:
TITLE OF INVENTION: Sequences and Antibodies
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 LeuAsnSerGlyTyrIleThrAlaThrAlaLeuLeuThrLeuSerCysGl 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 LeuAlaAspPheLeuLeuThrLysLys...PheArgLeuIleThrValAr 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325 laProArgTyrSerSerPheLeu 332
                                                                                                                                                                                                                                                                                  STREET: Two Embarca
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gLysIleAlaThrIleLeuGlySer.Leu........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCCAGGTAAGAGCTCTACCTG 20708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGCCTCCAGTTACGTGATAACCATTATTTTGCTGATACTTATTCCTGG 20781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yLeuSerThrLeuCysGlnSerGlyIleTyrIleAsnValLeuAspIleA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......ProSer.SerAlaLeuIleValSerLeuProTyr 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feder, John N.
Kronmal, Gregory S
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                                                                                                         #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              5872237e1
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alignment_block:
US-09-391-958-1 x US-08-724-394A-21/rev
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Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-724-394A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
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                                                                                                                                                                                             21980
                                                                                                                                                                                                                                                                                                                                               22080 TTCTTTCAGCCCAGTTCTCCTGGACGAGCTGTCCCCATAAAGGCGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22280 GTTCACAGTGATTTATGATGACCCCATGCATCACCCGTGCATAAGTGTTA
                                                                                                                                                                                                                                                                      22030 TCACATGCCTACCACTTTGGGCCATTTTCCTGGGTTTTTTCAGCCATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                22130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22180 CCTTGTACCTGTGGCCCATGCAGAGGTCTCTAGGGCAGGGTGTGGATCTC
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                                                                                                                                                      227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                               211 TrpLeuValSerThrMetValValTyrIleProThrTyrIleSerSerVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 erGluLysGluTyrIleIleSerSerLeuLysGlnGlnValGly..... 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 pPheValValIleTyrAspAspProValSerTyrProTrpIleSerThrS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 PheTyrIlePhe......GlyGlyValGlyCysValCysCysLeuTeuTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1..246240 OTHER INFORMATION: /no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
TOPOLOGY: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                  AATGATAATGGTAATAAGGAGAAACAGTTCTGTGTTACCTATTACATTCT 21831
                                                                                                             GCTCCATGTTAACATCAGAGATGTGAGTTTACTTCCTATACTTCTACGAA 21881
                                                                                                                                                                                             TGGTTGTGCACCATCATCCTAACATACCTACCAACGTATATCAGTACTCT
                                                                                                                                                                                                                                                                                            euArgSerLeuProIleTrpSerIleCysLeuGlyCysPheSerHisGln 210
                                                                                                                                                                                                                                                                                                                                                                                       .....LeuProIleLysAlaMetL 194
                                                                                                                                                                                                                                                                                                                                                                                                                            CTCTGAGAGGCACCATCTTGGCTGCTCTAATACTCATGCTGATTAGATCT 22081
                                                                                                                                                                                                                                                                                                                                                                                                                                                             rSerLysGln..Pro.....
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1.848
29.650
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                                                                                                                                                      234
234
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                                                                                                                                                                                                                                                                      21981
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alignment_scores:
US-08-724-394A-22
: 1246240
; NAME/KEY: misc_feature
; FEATURE:
GY: not
ESS:
acid
; LENGTH: 246240 base pairs
; INFORMATION FOR SEQ ID NO: 22:
; TELEFAX: 415-576-0300
; TELEPHONE: 415-576-0200
: TELECOMMINICATION INFORMATION:
REGISTRATION NUMBER: 35,136
; NAME: Fitts, Renee A.
; ATTORNEY/AGENT THEORMATTON:
1-OCT-1996
; APPLICATION NUMBER: US/08/724,394A
; SUFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA:
SYSTEM: PC-DOS/MS-DOS
BM PC C
COMPUTER READABLE FORM:
4
COUNTRY: USA
; CITT: San Francisco :
wo Embarcadero Center, 8th Floor
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
NVENTION:
INVENTION: Megabase Transcript Map: No 587
Tsuchiha
Thomas, Winst
; APPLICANT: Ruddy, David A.
Kronmal, Greg
Feder, John N.
<pre>seq_documentation_block: Sequence 22, Application US/08724394A</pre>
<pre>seq_name: /cgn2_6/ptodata/1/ina/5C_COMB.seq:US-08-724-394A-22</pre>
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292 LeuAsnSerGlyTyrIleThrAlaThrAlaLeuLeuThrLeuSerCysGl 308 ::: ::: ::: 20830 GTGGCCTCCAGTTACGTGATAACCATTATTTTGCTGATACTTATTCCTGG 20781
20880 ATTGCCCAGGGCTCCTTCCATCAATATGTGCTGTGGCCCTGCCCCTTT 20831
281

Quality: Ratio:

297.50 1.848

Length: Gaps:

Percent Similarity: 29.650 Percent Identity: 20.994	
alignment_block: US-09-391-958-1 x US-08-724-394A-22/rev	
Align seg $1/1$ to reverse of: US-08-724-394A-22 from: 1 to:	
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151 pPheValVallleTyrAspAspProValSerTyrProTrpIleSerThrS 16 :::	
168 erGluLysGluTyrIleIleSerSerLeuLysGlnGlnValGly 18	82 2181
183se 1	83
~ 6	87
CTCTGAGAGGCACCATCTTGGCTGCTCTAATACTCATGCTGATTAGATCT 2	2081
188LeuProIleLysAlaMetL 19 :::	94
194 euArgSerLeuProIleTrpSerIleCysLeuGlyCysPheSerHisGln 21 ::	1981
211 TrpLeuValSerThrMetValValTyrIleProThrTyrIleSerSerVa 22	127 11931
227 lTyrHisValasnileArgAsp	1881
234 23	34
21880 AATGATAATGGTAATAAGGAGAAACAGTTCTGTGTTACCTATTACATTCT 218	1831
	34
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234	134 1731
234	34
21730 GAGATAACTTGCCCCAGGTTGCACAATACTAAGTGATAGAGCTGCTGCAG 21	1681
234 23	
21680 CATCCATATTCTTAACCACTATGCTATACTACCACCACCAGCTGATTCCAA 21	1631
234	34
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21.500 - TABATHAD ACCUPATION OF THE TOTAL OF	1531
234	4

20780 325 20730	292 20830	2081 2081	209	209	210: 210:	23 2108	2 211	211	2	212:	2:	212	N) i		2131	2:	214:	2:	2141	2	215:
		281ProSer.SerAlaLeuIleValSerLeuProTyr 291	930 AATCCCTTTTCTGCACATGGTCTCAGAGGGTTCCCTGACAGCATGTCCTC 20881	9LysIleAlaThrIleLeuGlySer.Leu	256 LeualaaspPheLeuLeuThrLysLysPheargLeuIleThrValar 271 	239 eralaLeuProPheIleValAlaTrpValIleGlyMetValGlyGlyTyr 255 ::: ::: 080 CCTCCCTGCCTTTTATTGCTGCTGCAAGCTGTACAATTTTAGGAGGTCAG 21031	235AsnGlyLeuLeuS 239 ::: ::: 130 TCTCTATAACTACTCTGTATAAACTTCCTTCCTTCAGAGTGGAGTTCTGT 21081	.180 GGTAAGTTAATGGCTGGTCTGTGTAACTGACAAATTTTGGTGCTAACGTA 211.31	234	230 GTGTGAAAAAGGATGCTAATTTTCCCCCCAAACAACCCACAGTATCATGGG 21181	234 234	CCCAGAGTGATGCAGCTTCTGGCCCCTCTTATCTGAGACAGTGTTCTTTTA		234	380 TGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGCGACAGAGTAAGACT 21331	234 234	30 AGGAGGCTGAGACAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAT 21381	234 234	.480 TACAAAATTAGCCAGGTGTGGTGGCAGGCACCTGTAATCCCAGCTATTC 21431	234 234	30 TGCAAGACCAGCCTGACCAATATGGTTTACTAAATATCATCTACTAAAAA 21481

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Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein -
      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB DB
    254.5
252.5
250.5
247.5
247.5
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244.244
244.2243
243.229.5
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279.5
278.5
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ALIGNMENTS

RESULT A48916

C;Genetics: C;Gene: GDB:SLC17A1; NPT1 A;Gene: GDB:SLC17A1; NPT1 A;Cross-references: GDB:141889; OMIM:182308 sodium phosphate transport protein 1, renal - human (Species: Homo sapiens (man) (C; Species: Homo sapiens (man) (C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999 (C; Accession: A48916 R; Chong, S.S.; Kristjansson, K.; Zoghbi, H.Y.; Hughes, M.R. Genomics 18, 355-359, 1993 (Genomics 18, 355-359, 1993 A; Title: Molecular cloning of the cDNA encoding a human renal sodium phosphate transp A; Reference number: A48916; MUID:94117004 A; Accession: A48916 δÃ 밁 Qy Вb δÃ В Qy 밁 Qγ Вþ QΥ 밁 δÃ A;Molecule type: mRNA A;Residues: 1-467 <CHO> A;Cross-references: GB:X71355; NID:g450531; PIDN:CAA50490.1; PID:g450532 A; Status: preliminary Matches 193; Query Match 181 121 361 116 GCFTAILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYIIS 61 61 SEVL------PVDSFGGLSKAPKSL------Match 46.48; Local Similarity 41.38; 1 MQVDETLIPRKVPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDS GYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFL GPFIVLLVTGVICESLGWPMVFYIFGACGCAVCLLWFVLFYDDPKDHPCISISEKEYITS LSLLIPPAAGIGVAWVVVCRAVQGAAQGIVATAQFEIYVKWAPPLERGRLTSMSTSGFLL TFYSIVIFLILAGATGSFCLGGVFINGLDIAPRYFGFIKACSTLTGMIGGLIASTLTGLI TKKLLDNIKNPMYNWSPDIQGIILSSTSYGVIIIQVPVGYFSGIYSTKKMIGFALCLSSV 120 MQMDNRLPPKKVPGFCSFRYGLSFLVHCCNVIITAQRACLNLTMVVMVNSTDPHGLPNTS 60 Conservative 68; Mismatches 140; Indels 66; Score 964; DB 2; Pred. No. 1.8e-69; Length 467; Gaps 175 294 300 180 80 240 w ••

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RESULT 3
139473
Na+-dependent phosphate cotransporter - human C; Species: Homo sapiens (man)
C; Date: 29-May 1998 #sequence_revision 29-May C; Accession: 139473
R; Miyamoto, K; Tatsumi, S.; Sonoda, T.; Yaman Biochem. J. 305, 81-85, 1995
A; Title: Cloning and functional expression of A; Reference number: 139473; MUID:95126933
A; Accession: 139473
A; Status: preliminary; translated from GB/EMBI A; Molecule type: mRNA
A; Residues: 1-465 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sodium-phosphate transport system 1 - mouse C;Species: Mus musculus (house mouse) C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_ch C;Accession: S69915
R;Chong, S.S.; Kozak, C.A.; Liu, L.; Kristjansson, K.; Dunn Am. J. Physiol. 268, 1038-1045, 1995
A;Title: Cloning, genetic mapping, and expression analysis A;Reference number: S69915
A;Accession: S69915
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Pred. No. 4.8e-68;
8; Mismatches 134
                          from GB/EMBL/DDBJ
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A; Cross-references: GB:D28532; NID:g639841; PIDN:BAA05888.1; PID:g639842
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QDPESAWFKTFILMAAINVTGLIFYLIVATAEIQDWAKEKQHTRL
                                                                                             YSIVIFLILAGATGSFCLGGVFINGLDIAPRYFGFIKACSTLTGMIGGLIASTLTGLILK 420
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sodium/phosphate transport protein, renal - rabbit N;Alternate names: sodium/phosphate cotransporter C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #tc C;Accession: A56410; S27951
R;Werner, A; Moore, M.L; Mantei, N; Biber, J; Seme Proc. Natl. Acad. Sci. U.S.A. 88, 9608-9612, 1991
A;Title: Cloning and expression of cDNA for a Na/P-1 cA;Reference number: A56410; MUID:92052140
A;Accession: A56410; MUID:92052140
A;Accession: A56410; A;Cross-references: GB:M76466; NID:g165689; C;Keywords: kidney; transmembrane protein VDETLIPRKVPSLCSARYGIALVLHFCNFTTIAQNVIMNITMVAMVNSTSPQSQLNDSSE 62 KRLDNTKNPVYNWSPDVQGIIFSSIFYGAFLIQIPVGYISGIYSIKKLIGFALFLSSLVS MDNQFPSRKGPCFCSFRYVLALFMHFCNIVIIAQRMCLSLTMVAMVNNTNLHGSPNTSAE 60 Conservative 44.98; 77; -AKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGC Score 932; DB 2; Pred. No. 6.2e-67; Mismatches 139; -VLPVDSFGGLSKAPKSLP PIDN: AAA31461.1; Na/P-1 cotransport Semenza, #text_change 05-Nov-1999 Length Indels G.; PID:g165690 Murer, 66; system Gaps 81 of. kidney Ψ

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                                                WRNVFFLLFAVNLLGLLFYLIFGEADVQEWAKERKLT
                                                                                                                               LTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTYSGFLLSQDPEFG
                                                                                                                                                                                                                                                                                                          TKFNTPWRRFFTSMPVYAIIVANFCRSWTFYLLLISQPAYFEEVFGFEISKVGLVSALPH
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  WQYVFLIASLVHYGGVIFYGVFASGEKQPWAEPEEMS
                                                                                                    LVLAVGFSGFAISGFNVNHLDIAPRYASILMGISNGVGTLSGMVCPIIVGAMTKHKTREE
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Pred. No. 2.2e-30;
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RESULT 6
T23589
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T23580
hypothetical protein K10G9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text
C;Accession: T23589; T24636
R;Mortimore, B.
R;Mortimore, B.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library
A; Reference number: Z19915
A; Accession: T24636
A; Status: preliminary; translated
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A;Accession: T23389
A;Status: preliminary; translated
A;Molecule type: DNA
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A;Map position: 3
A;Introns: 38/3; 87/3; 224/1;
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A; Residues: 1-573 <WI2>
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A; Residues: 1-573 <WIL>
A; Cross-references: EMBL: Z36282;
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Best Local :
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                PTVSGFTLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIFGEADVQEWAKE
                                                              CLAFVRDPVIAVTELI-IACSGAGAVLSGENVNHEDIAPRHAPILMGIANGLGAIAGV-G
                                                                                   SLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIV
                                                                                                                                VGVMVGLPASAYLVSHFSWSTPFYVFGALGIVWSILWIYVSGTSPETHGYISADEKKYI-
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                                                                                                                                                                  HVNIRDNGLLSALPFIVAWVIGMVGGYLADFLLTK-KFRLITVRKIATILGSLPSSALIV
                                                                                                                                                                                                    ---TEKVGSVAVKNMTLTTLPWRDMMTSTAVWAIIICSFCRSWSFFLLLGNQLTYMKDVL
                                                                                                                                                                                                                                      SSLKQQVGS-----SKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSVY
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ce: clone T07A5
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Pred. No. 2.6e-28;
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hypothetical protein T07A5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T24633

15-Oct-1999 #text_change 15-Oct-1999

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C; Genetics:
A; Introns: 5
C; Keywords:
                                                                                                                                                                                                                                                                                                                                                             RESULT 8
528286
Sypothetical protein C38C10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #te
                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-472 < THO>
                                                                                                                                                                                                                                                              A; Reference number: A; Accession: S28286
                                                                                                                                                                                                                                                                              submitted to the EMBL Data
A:Reference number: S28285
                                                                                                                                                                                                                                                                                                                                 R; Thomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Buck, D.

R;Buck, D.

R;Buck, D.

R;Buck D.

R;Reference number: Z19915

A;Accession: T24633

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-544 <WIL>
A;Cross-references: EMBL:Z48055; PIDN:CAA88134.1; GSPDB:GN00021; CESP:T07A5.3

A;Experimental source: clone T07A5

C;Genetics: Table Communication of the communication of 
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A;Map position: 3
A;Introns: 38/3; 87/3;
                                                                                                                                                    Genetics:
Introns: 50/3;
                                                                                                                                                                                             Cross-references: EMBL:Z19153
                       Matches
                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                      Accession: S28286
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 VPTVSGELLSQDPEFGWRNVFFLLFAVNLLGLLFYLLFGEADVQEWAKE 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFGSIAPV---I 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIKNSGFISIFPQFGMCIVTLATGQLCDYLRSSGKMSTEAVRKSVNTFGFTVEAMMLGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TEKIGDVAVKNMSLTTLPWRDMMTSSAVWAIIICTFCRSWGFFLLLGNQLTYMKDVLHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFTAILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIXDDPVSYFWISTSEKEYIISS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AFVRDPVIAVTCLV-IACTGSGSVLSGFNVNHFDIAPRYAPILMGIANGLGAVAGVGGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKQQVGS-----SKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSYYHV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLND-----SSEVLPVDSFGGLSKAPKSLPAKSSILGGQFA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAISFNFHPYTDIFVMVVQAVQGLALGVLYPAMHGVWKFWAPPLERSKLATTAFTGSSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTITEQKKFFLRKVRWQIAILAHFGFAISFGIRSNF-GVAKNRMVN-----NFTDAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVHEREFLWTGAEVGMMESSFFYGYAASQIPA--GVLAAKFAPNKIFMLGILVASFMNIL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETLIPRKVPSLCSARYGIALVLHF------CNFTTIAQNVIMNITMVAMVNSTSPQS 55:1: :1 | | ::| ::| | |
                                                                                                                            transmembrane
                                         Similarity
                                                                                                                        287/3; 351/3; 412/3
smembrane protein
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                       20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.9%; Score 434; DB 2; 25.4%; Pred. No. 3.9e-27;
                                                                                                                                                                                                                                                                                                        Library,
                  83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 429; DB 2; Length 472; Pred. No. 8.3e-27; Mismatches 162; Indels
                                                                                                                                                                                                                                                                                                        December 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
             36;
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         Gaps
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A;Introns: 79/3; 115/3; 128/3; 200/3; 288/3;
A;Note: A_IG005I10.nn
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A; Residues: 1-413 <AND>
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A;Description: The sequence of A. thaliana
A;Reference number: Z14347
A;Accession: T01534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVFFLLFAVNLLGLLFYLIFGEADVQEWAK 394
                                                                                                                                                                                                                                                                                                                                                                                                       106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T01534
                                                                                                                                                                                                                                                                                                                                                                                                18.7%; Score 388; DB 2; ilarity 25.7%; Pred. No. 1.3e-23; Conservative 69; Mismatches 133
-NIRDNGLLSALPFIVAWVIGMVGGYLADFLLTKKFRLITVRKIATI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG005110
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RESULT 9
T01534
T01534
hypothetical protein A_IG005110.nn - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_0
                                                                                                                                                                                                                                                                                                                                                              19 RYGIALVLHECNETTIAQNVIMNITMVAMVNSTSPQSQ-LNDSSEVLPV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 GWPSIFYIIGVFGVLWTAVWWYVSSDKPATHPRITPEEKQYIVTAVEASMGKDTGKVPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 A--TFPA-----MHTMWSVWGPPLELSVLTGVTYAGAQIGNVIVLPLSGFLCEYGFDG 181
K-----PREPVTVIPWKLILSKPPVWALIISHFCHNWGTFILLTWMPTYYNQARSSASVI
                                                                                                                                                      FTAILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYIISSL
                                                                                                       VTGLAFSPMLITKFGWPSVFYSFGSLGSIWFLLWLKFAYSSPKDDPDLSEEEKKVILGGS
                                                                                                                                                                                                             TQILGGIWADKFGGKGVA---MPAMNNML-----SKWIPVSERSRSLALVYSGMYLGS
                                                      KQQVGSSKQP----LPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTY-----I
                                                                                                                                                                                                                                                                                                               RRWVIVLLCFSSF-----LLCNMDRVNMSIAILPMSQEYNWSSATVGLIQSSFFWGYLL
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                                                                                                                                                                                                                                             ------DSFGGLSKAPKSLPAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLIGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG--LSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDPEFGWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --IKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSVYHVNIRDNGLLSALPFIVAW 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGMAISGLQYAGFVVNYLEIAPPFSGTVMGTGNTISALAGIISPAVSSYLTPNGTQEEWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASRYGGKRVV----FVT-----ILGSALLTLLNPVAART----SEYALAILRAAIGFLQG 130
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hypothetical protein F12B6.2 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t C;Accession: T15201 R;Pauley, A.; Maggi, L.
                                                                                   RESULT
T15201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R:Kershaw, J.
submitted to the EMBL Data Library,
A:Reference number: Z19929
A:Accession: T24729
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                                                                                                                                                    В
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A; Introns: 85/1; 143/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-516 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T09B9.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t C;Accession: T24729
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Best Local S
Matches 105
                                                                                                                                                      423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                    FSIFNKLLISQILRTGSKHEWTIVFEISAFVAILPTIFFTLWGSAERTEWASNR 476
                                                                                                                                                                                  APVIVPTVSGFLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIFGEADVQEWAKER 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNHPKQFAWSSIQQGLIYSGQNFGSLFMVITGWQADRLNGKWTIVAAMAFIIVSNAVLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CN-----FTTIAQNVI---MNITMVAMVNSTSPQSQLND------SSEVLPV
                                                                                                                                                                                                                  CIAATPLMSNLQHAIWAIIILCLANAFAGLHTPGVLTAIVQLAPAFSGIITGLAFAVASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAGASFALVFFLRVLTGFGDALLS-PASSSLI-----TRWFPPKERFSALGIVTSGRQ
                                                                                                                                                                                                                                                   LIVSLPYLNS--GYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSI
                                                                                                                                                                                                                                                                                  DVLGLSNTVNGLVSALPMAILFLSKCLSASLASYLTANGYLRKTQSCKIFNFIASLGLGI
                                                                                                                                                                                                                                                                                                                  SVYHVNIRDNGLLSALPFIVAWVIGMVGGYLADFLLTKKF-RLITVRKIATILGSLPSSA
                                                                                                                                                                                                                                                                                                                                                                                  EKEYIISSLKQQ-VG--SSKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYIS
                                                                                                                                                                                                                                                                                                                                                                                                                  IGTLIILPIGGWLCGSDGSKFLGGWPAIFYLSSVVAAAVLVIWVVFSADKPSKHLCISHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D---SFG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTAGVLAGVEGTAATGXILQRG---SWDDVFKVAVALXLIGTLVWNLFATGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGFSSIAPVIVPTVSGFLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIFGEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEAYINRKIEEENIGKRNNRKNTPWKAIFTSKQVWVAVAALVCHEFPLVIMLQFLPKFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGCFTAILIGGFI-----SETL-GWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184/1; 241/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GLSKAPKSLPAKSSILGGQFAIWERWGPPQERSRLCSIALSGML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 320; DB 2
Pred. No. 4.5e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         344/1; 391/1; 436/2; 470/3
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                                20-Sep-1999 #text_change
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-18;
177;
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A; Gene: CESP:F21F8.11
A; Map position: 5
A; Introns: 16/1; 64/2; 112/3; 344/3; 417/1; 452/1
                                                                                                                                                                                                                                                                                                                                                                               R; Wilson, R.; Favello, A.; Le, T.T. submitted to the EMBL Data Library, April A; Description: The sequence of C. elegans A; Reference number: 220618
                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F21F8.11 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te C;Accession: T29418
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A; Map position: 1
A; Introns: 23/1; 62/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans co:
A;Reference number: Z18307
A;Accession: T15201
                                 Q
                                                                                                                                                                                                                                                            A;Molecule type: DNA A;Rosidues: 1-530 <WIL> A;Rosidues: 1-530 <WIL> A;Cross-references: EMBL:U97000; PIDN:AAC47997.1; GSPDB:GN00023; CESP:F21F8. A;Experimental source: strain Bristol N2; clone F21F8
                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z20618
A; Accession: T29418
A; Status: preliminary; translated
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A; Residues: 1-499 < PAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 24.5
Matches 80; Conservative
                                                                             Query Match 14.7
Best Local Similarity 22.9
Matches 110; Conservative
                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445
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MCQMTAHIGLSLSCMCNSTAVA---LMNTNNATLVEGTESTILMSILENKTSESQELGGG
                                     LCSARYGIALVLH-FCNFTTIAQNVIMN------ITMVAMVNSTSPQSQLNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIYEWKCAFYSLAGVLAVTGLIFQIFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMLRSLP-----IWSICLGCFSHQWLVSTMVVYIPTYISSVYHVNIRDNGLLSALP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYIISSLKQQVGSSKQPLPIK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPAGSVLISS-----WFPLSEKSTAMAIFTTGNQIG----IAVSMFLTAKLCQLHFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEFGWRNVFFLLFAVNLLGLLFYLIFG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQLSIIVSMAAFSAYVPGYNTSIVTVAPQFTAFISSYAQLYAQIASTLAPIVIGRITSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTLSCGLSTLCQS----GIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GWPLVFIVYGLIGAVFLVIWHVRLADKPRESKYITATELTYI-----KGGKQRRNRAE
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                                                                                              14.7%;
22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.8%; Score 306.5; DB 2; 24.5%; Pred. No. 5.2e-17; Live 72; Mismatches 134;
                                                                               69;
                                                                             Score 304.5; DB 2;
Pred. No. 8e-17;
9; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                              from
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                                                                                                                   Length
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hypothetical protein ZK682.2 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
C; Accession: T29968
R; Du, Z.; Le, T.
submitted to the EMBL Data Library, November 1995
A, Description: The sequence of C. elegans cosmid ZK682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Rosidus: 1-506 < DUZ> A;Cross-references: EMBL:U41110; PIDN:AAA82415.1; CESP:ZK682.C;Genetics: A;Gene: CESP:ZK682.2 A;Introns: 37/3; 82/3; 163/3; 314/3; 359/1; 469/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: The sequence A; Reference number: 220714 A; Accession: T29968
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LIC--LAMCFVSGYIPGYNTSAVTIAPGQTAAIAAFSRFWGQIASSVAPYHIGAYTKQGT
                                LSCGLSTLCQSGIYI-----NVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDP
                                                                       VFYAGMAE---SARKRDWSDINRITKFCNSSASFGIAICFGLLCLCDCSQRG-----AAIF
                                                                                                                                                                                 KAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSVYHVNIRDNGLLSALPFIVAWVIG
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                                                                                                        MVGGYLADFLLTKKFRLITVRKIATILGSLPSSALIVSLPYL-----NSGYITATALLT
                                                                                                                                            MALMKSPVVWAIAASSFAHNYVTVGTITYLPLYYKTVLNMSLTSNGLWSALPFVLQLISK 330
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                                                                                                                                                                                                                                                                                                                                                                      70;
                                                                                                                                                                                                                                                                                                                                                                      Score 282.5; DB 2;
Pred. No. 4.3e-15;
0; Mismatches 140;
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RESULT 14
S44742
C02C2.4 protein - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-5
C; Accession: S44742
R; Wilson, R.
submitted to the EMBL Data Library, September 1993
A; Description: Sequence of the C. elegans cosmid C02C2.
               A; Molecule type: DNA
A; Residues: 1-420 < DUZ>
                                                                    submitted to the EMBL Data A; Description: Sequence of A; Reference number: S44613 A; Accession: S44900
                                                                                                                                          RESULT 15
$44900
ZK652.10 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change
C;Accession: $44900
R;Du, Z.
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A; Residues: 1-568 <WIL>
 A; Cross-references:
                                                     A; Status: preliminary
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| 92; Conserv
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EMBL:L14429; NID:g289765; PID:g289766
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the C. elegans co
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Pred. No. 7.8e-15;
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A;Introns: 60/1; 104/3; 155/3; 200/1; 230/2; 281/3; 337/1; 354/3; 379/1
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177 GIDKLKENKILSNTKAVKVSHGVASFGSSFSLILLAFFVDCSNPTTGLIFFCLMYSSMGT 236
                                                                                                                                          256 LADFILITKKFRLIT-VRKIATILGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTL-- 313
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                                                                                                                                                                                                                                                58 FAGIFATGWSILWFFTASSHPAKVKMMTKKEKEYLLANVVKKVHKSEKTRSIPYSKILTS 117
                                                                                                                                                                                                                                                                                                                                     80 PAKSSILGGQFAIWERWGPPQERSRLCSI-ALSGMLLGCFTAILIGGFISETLGWPFVFY 138
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Search completed: May 25, 2000, 14:27:17 Job time: 2304 sec

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                                                                                                                                                                        transporter from human kidney: expression."; Biochem. J. 305:81-85(1995).
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Miyamoto K.-I., Tatsumi S.,
Taketani Y., Takeda E.;
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Matches 191;
NPT1_RAT STANDARD; PRT; 465 AA. 662795; 62795; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 1 (SODIUM/PHOSPHATE COTRANSPORTER 1) (NA(+)/PI COTRANSPORTER 1) (RENAL SODIUM-PHOSPHATE TRANSPORTER 1) (RENAL SODIUM-PHOSPHATE COTRANSPORTER 1) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 1).
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modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (
Eukaryota; Metazoa;
Eutheria; Rodentia;
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LSSLPYLLAYICGIVAGQMSDFLLSRKIFSVVAVRKLFTTLGIFCPVIFVVCLLYLSYNF
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a; Chordata; Craniata; Vertebrata; Mammalia;
a; Sciurognathi; Muridae; Murinae; Rattus.
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Pred. No. 6.5e-65;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 1 (SODIUM-PHOSPHATE
COTRANSPORTER 1) (NA(+)/PI COTRANSPORTER 1) (RENAL SODIUM-PHOSPHATE
TRANSPORT PROTEIN 1) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 1).
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Bourdeau J.E., Hughes M.R.;
"Cloning, genetic mapping, and expression
                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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sodium-dependent phosphate cotransporter.";
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Eukaryota; Metazoa;
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FUNCTION: IMPORTANT FOR THE RESORPTION OF PHOSPHATE MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE NA+ COTRANSPORT IN THE RENAL BRUSH BORDER MEMBRANE.
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Metazoa; Chordata; Craniata; Vertebrata;
Mentia; Sciurognathi; Muridae; Murinae;
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FUNCTION: IMPORTANT FOR THE RESORPTION OF BHOSPHATE I MAY BE INVOLVED IN ACTIVELY TRANSPORTING PHOSPHATE I NAY BE COTRANSPORT IN THE RENAL BRUSH BORDER MEMBRANE.
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Oryctolagus cuniculus (Rabbit).
Pinkaryota; Metazoa; Chordata; Craniata; Vertebrata;
Pinkaryota; Metazoa; Chordata; Oryctolagus.
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15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 1 (SODIUM-PHOSPHATE
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TISSUE=KIDNEY CORTEX;
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases i- EUNCTION: MAY BE INVOLVED IN ACTIVELY TRANSPORTING INTO CELLS VIA NA+ COTRANSFORT (BY SIMILARITY).
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 3
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roria: Primates; Catarrhini; Hominidae; Homo.
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  Peloderinae;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO MAMMALIAN SODIUM/PHOSPHATE COTRANSPORTER 1.
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                                                          APRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIF
                                                                                                                                  RLIT-VRKIATILGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDI
                                                                                                                                                                                              NFARSWTFYLLLQNQLTYMKEALGMKIADSGLLAAIPHLVMGCVVLMGGQLADYLRSNKI
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                  APRYAAILMGFSNGIGTLAGLTCPFVTEAFTAHS-KHGWTSVFLLASLIHFTGVTFYAVY
                                                                                                      LSTTAVRKIFNCGGFGGEAAFMLIVAYTTSD-TTAIMALIAAVGMSGFAISGFNVNHLDI
                                                                                                                                                                                                                                                                                    FCVTFEKPAFHPTISQEEKIFI----EDAIGHVSNTHPTIRSIPWKAIVTSKPVWAIIVA
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RESULT 8
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01-NOV-1997
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Silms M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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Rhabditina; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                             Jones S.J.M.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-i- SIMILARITY: TO MAMMALIAN SODIUM/PHOSPHATE COTRANSPORTER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                elegans
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                                                                                                                                                                                                                               WORMPEP;
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European Bioinformatics Institute.
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S28286; S28286.
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, Last annotation update)
PROTEIN C38C10.2 IN CHROMOSOME
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Rhabditidae; Peloderinae; Caenorhabditis.
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                          Length 493;
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 Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: TO MAMMALIAN SODIUM/PHOSPHATE COTRANSPORTER 1.
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                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                            Rhabditina;
                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans
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                                                                               Hypothetical Sodium transp
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; Rhabditoidea;
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5 KD PROTEIN T07A5.3 II
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Latreille P., Lightning J., Lloyd C., Mortingen B., O'Callaghan M.,
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MEDLINE; 94150718.
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Caenorhabditis elegans.
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28, Last sequence update)
35, Last annotation update)
KD PROTEIN CO2C2.4 IN CHROMOSOME
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                                      A., Weinstock L., Wilkinson-Sproat
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Rhabditidae; Peloderinae; Caenorhabditis.
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Pred. No. 1.1e-25;
5; Mismatches 167
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GUDT_ECOLI Q46916; 15-JUL-1998 15-JUL-1998 15-JUL-1998

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-i- SIMILARITY: TO MAMMALIAN SODIUM/PHOSPHATE COTRANSPORTER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Sodium transp
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les 92; Conserv
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SMFRKDGTAAEWQNIFIGCSLAHIFSGSIFLLFGSGELQDWAK
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                       GFLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIFGEADVQEWAK
                                                                                                                                                 VKKVHKSEKTRSIPYSKILTS-PAFLGQLQCHFFVNLFMTLFQIYLPSYFKEVLHLGVIA
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                                                DCSNPTTGLIFFCLMYSSMGTFVSGFYTSLLSLAPQYTATMSAISMFVAMIGRLTTPAVM
                                                                        SGYITATALLTLSCGLSTL--CQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVS
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Mismatches 191;
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STRAIN-K12 / MG1655;
MEDLINE; 97426617.
Blattner F.R., Plunkett G
Riley M., Collado-Vides J
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTE:
-!- SIMILARITY: BELONGS TO THE PHTHALATE PERMEASE FAMILY.
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Mau B., Shao Y.;
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                                              SODPEFGWRNVFFLLFAVNLLGLLFYLI
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EG13169; YGCZ.
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nilarity 24.7%;
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J., Glasner F.D., Rode C.K., Mayhew G.F.,
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Pred. No. 4.8e-14;
4; Mismatches 140;
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Blattner F.R., Plunkett
Riley M., Collado-Vides
Gregor J., Davis N.W., K
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                        SALPFIVAWVIGMVGGYLADFLLTKKFRLITVRKIATILGSLPSSALIVSLPYLNSGYIT
ASIPALCGFAGGVLGGVFSDYLIKRGLSLTLARKLPIVLGMLLASTIIL-----CNYTN
                                                                         SAAASGPKLHYIKQLLSNRMMLGVFFGQYFINTITWFFLTWFPIYLVQEKGMSILKVGLV
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s J., Glasner F.D., Rode C.K., Mayhew G.F.,
Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
"Determination of a 21548 bp nucleotide sequence around t
degrees region of the Bacillus subtilis chromosome.";
Microbiology 141:269-275(1995).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-i- SIMILARITY: BELONGS TO THE PHTHALATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                         Hypothetical protein; TRANSMEM 19 3
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                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
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Bacteria; Firmicutes;
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01-JUL-1993
15-JUL-1998
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                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                    Unpublished observations (OCT-1993).
-!- FUNCTION: INTAKE OF GALACTONATE INTO THE CELL.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                         Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R., "DNA sequence and analysis of 136 kilobases of the Escheric genome: organizational symmetry around the origin of replic Genomics 16:551-561(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12 / MG1655;
MEDLINE; 93315143.
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                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                              (PROBABLE).
-!- SIMILARITY: BELONGS TO THE PHTHALATE PERMEASE FAMILY.
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NE; EG11715; DGOT
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(Rel. 26, Last sequence up
(Rel. 36, Last annotation
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Best Local Similarity
Matches 85; Conser
                                                                                                                                                    STRAIN-K12 / MG1655;

MEDLINE; 97426617.

Blattner F.R., Plunkett G

Riley M., Collado-Vides J

Gregor J., Davis N.W., Ki

Mau B., Shao Y.;
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P39398; P39397;
01-FEB-1995 (Rel.
15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
HYPOTHETICAL 49.4 I
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SEQUENCE
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STRAIN=K12 / MG1655;
MEDLINE; 95334362.
Burland V.D., Plunkett G.
           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and its content is modified and this statement is not removed.
                                                                                                                                       "The
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                                                                                                                                                                                                                                                                    "Analysis of the Escherichia coli genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
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                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). SIMILARITY: BELONGS TO THE PHTHALATE PERMEASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIFEAP-AFPINNRMV-----TSWFPEHERASAVGFYTSGQFVGLAFLTPLLI--WIQ 179
                                                                                                                          complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TALKAGEMTTVPELAAFVGVLLSGWVADLLVRKGESLGFARKTPIICGLLISTCIMGANY
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statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/
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PROTEIN IN TSR-MDOB
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s J., Glasner F.D., Rode C.K., Mayhew
Kirkpatrick H.A., Goeden M.A., Rose I
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U14003; AAA97253.1; A
AE000506; AAC77312.1;
                                                                                             ALPFIVAWVIGMVGGYLADFLLTKKFRLITVRKIATILGSLPSSALIVSLPYLNSGYITA
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FIV--DTTHSFRLALIICGCVTAAGALAYIFLVRQPINDPRKD
                   FLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIFGEADVQEWAKE
                                        TAVLLIGMALFCIHFAGTSCWGLIHVAV --
                                                         TALLTLSCGL-----STLCQSGIYINVLDIAPRYSSFLMGASRGFSS-IAPVIVPTVSG
                                                                               AIPFLFGAAGMLVNGYVTDWLVKGGMAPIKSRKICIIAGMFCSAAFTLIVPQATT---
                                                                                                                                                                ------MGWRGMFITIGVLGIFLAIGWYMLYRNR--EHVELTAVEQAYLNAG----SVN
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43 6;
72 9;
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Submitted (SEP-1997) to the EMBL/Ge
-!- SUBCELLULAR LOCATION: INTEGRAL
EMBL; AR024691; AAC39088.1; -.
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Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila ananassae (Fruit fly).
Eukaryota; Metazoa; Arthropoda; T
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LSMFISVIADWMISSKRFSLTATRKIINSIGQYGPGLALIAASYTGCDRALTLAILTIGV
                                                                                                                                                                                       FDGGWPSIFYVFGIVGTVWSIAFLIFVYEDPSTHPKIDEREKKYINESLWGTDVIKSPPI
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187 207
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, Last sequence upo
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NTEGRAL MEMBRANE PROTEIN.
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Pred. No. 3.3e-27;
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"Cloning and expression of a clowa encoding a brain-specific Na(+)-
dependent inorganic phosphate cotransporter.";
Proc. Natl. Acad. Sci. U.S.A. 91:5607-5611(1994).
EMBL; U07609; AAA19646.1; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No. 2.1e
66; Mismatches
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No. 2.1e-26;
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Q09932 Q09932; Q1-NOV-1996 (Q1-NOV-1996 (Q1-MAY-1999 (HYPOTHETICAL K10G9.1.

(TIEMBLrel. 01, Created)
(TIEMBLrel. 01, Last sequence update)
(TIEMBLrel. 10, Last annotation update)
L 63.6 KD PROTEIN K10G9.1 IN CHROMOSOME

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PRELIMINARY;

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Best Local Sim
Matches 125;
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MORTIMORE B., BUCK D.;
MORTIMORE B., BUCK D.;
Submitted (FEB-1995) to the EMBL/Ge
EMBL; Z36282; CAA885289.1; JOINED.
EMBL; Z48055; CAA881389.1; JOINED.
EMBL; Z48055; CAA88135.1; JOINED.
SEQUENCE 573 AA; 63610 MW; FOOE
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
ROUNSLEY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON
SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER
"AIRBIDOPSIS Thallana chromosome II BAC T27A16 genomic seque
"AIRBIDOPSIS TABLIANA CHROMOSOME II BAC T27A16 genomic seque
                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
727A16.25 PROTEIN.
727A16.25.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eudicoty; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                      082390;
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                                                                                                                 Arabidopsis.
[1]
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Eukaryota; Metazoa; Nem
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25; Conservative
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
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26.7%;
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Rhabditidae; Peloderinae;
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Pred. No.
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.5e-24;
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oderinae; Caenorhabditis.
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                                                                      MASON T.M.,
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Best Loc
Matches
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Q94886; O1-FEB-1997 (TrEMBLrel. 02, Created)
Q1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
Q1-NG-1998 (TrEMBLrel. 07, Last annotation update)
NA(+)-DEPENDENT INORGANIC PHOSPHATE COTRANSPORTER.
NAPI-T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; ACO
PFAM; PFO
SEQUENCE
                                                                                                                                                                                                 MACIVER B.;
Thesis (1997), University of I
EMBL, Y07720; CAA68992.1; -.
FLYBASE; FBgn0016684; NaP1-T.
SEQUENCE 524 AA; 58814 MW;
                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit Eukaryota; Metazoa; Arthropoda; Pterygota; Neoptera; Endopterygo
                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                            TISSUE-OVERIAN;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                             170
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                                                                                           G---SWDDVFTISVGLYLVGTVIWNLFSTGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101;
TLMTHAPTYFRLIHHWNIRATGFLSGLPHLMRMLFAYVFSIFADYLLRTDKMSRTNVRKL
                      TMVVYIPTYISSVYHVNIRDNGLLSALPFIVAWVIGMVGGYLADFLL-TKKFRLITVRKI
                                                            IXDDPVSYPWISTSEKEYIISSLKQQVGSSKQPLPIKAMLRSLPIWSICLGCFSHQWLVS
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                                              VFDSPAEHPRIADSERKFIEKSLGASIQGSKGPTPWKAIATSRPVWLNVVAQWGGIWGLF
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PF00083; sugar_tr; 1.
NCE 512 AA; 56498 M
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Pred. No. 1.1e-
66; Mismatches
                                                                                                                                         Score 404.5; DB Pred. No. 2e-21; 0; Mismatches 14
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.1e-23;
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01-JAN-1998
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             023065
                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1997) to the EMBL; AF013293; AAB62846.1; SEQUENCE 413 AA; 45791 MV
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STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WATERSTON R.;
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                                                                                                                                                                                                                        FTAILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYIISSL
                                                                                                                                                                                                                                                                                                                         W 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVSGMIGGMPGFISPFIVGQLTHNNQTIDAWKNV-FLLTSLMLTGSGILYVLFSESKLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GASRGFSSIAPVIVPTVSGFLLSQDPEF-GWRNVFFLLFAVNLLGL-LFYLIFGEADVQE
                                                                                                                            SSVYHV------NIRDNGLLSALPFIVAWVIGMVGGYLADFLLTKKFRLTTVRKIATI
                                                                                                                                                                                                        VTGLAFSPMLITKFGWPSVFYSFGSLGSIWFLLWLKFAYSSPKDDPDLSEEEKKVILGGS
                                                                                                                                                                                                                                                                                                           RRWVIVLLCFSSF------LLCNMDRVNMSIAILPMSQEYNWSSATVGLIQSSFFWGYLL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATILGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLM
NTAGVLAGVFGTAATGYILQRG---SWDDVFKVAVALYLIGTLVWNLFATGE
                        RGFSSIAPVIVPTVSGFLLSQDPEFGWRNVFFLLFAVNLLGLLFYLIFGEAD
                                                                                                    SLLFNIFCEQVLKFNLTESGLLCVLPWLTMAVFANIGGWIADTLVSRG-------
                                                                                                                                                      K----PREPVTVIPWKLILSKPPVWALIISHFCHNWGTFILLTWMPTYYNQARSSASVI
                                                                                                                                                                               KQQVGSSKQP----LPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTY------I
                                                                                                                                                                                                                                                           TQILGGIWADKFGGKGVA---MPAMNNML-----SKWIPVSERSRSLALVYSGMYLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATFICCGTKGLIVLALAYFGYNATAAIVLVTVATMLHGAVSSGPLASMVDLSPNYAGIVL
                                                                          LGSLPSSALIVSLPYLNSGYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGAS
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(TrEMBLrel. 05,
(TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                   -DSFGGLSKAPKSLPAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                           45791 MW; 0D120117 CRC32;
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25.7%;
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Last annotation
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Pred. No. 2.4e-20;
9; Mismatches 133;
                                                  LSITNGSDAFSQSGLYSNHQDIGPRYAGVLLGLS
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01-JAN-1998
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F25G6.7 PROTI
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BONFIELD J., BURTON J., CONNELL M., COPEST J., COOPER J.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNK
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WATERSTON R.; Submitted (SEP-1997) to the EMBL; AF022973; AAC25800.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Submitted (SEP-1997) to
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 368:32-38(1994).
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MEDLINE; 941507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SWRFMTSIMLCFCFGCVHLMNSNMGMAIVCMVNSSATYDNETYPENAAPLLDWSSDEQGY
  ALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDPE
                                                                                       FIVAWVIGMVGGYLADFL-LTKKFRLITVRKIATILGSLPSSALIVSLPYLNSGYI-TAT
                                                                                                                                                                                                                                                                          ETL---GWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYI-ISSLKQQVGS-
                                                                                                                                                                                                                                                                                                                       GFADALLQPAMNSLI-----TRWFPTSERSYALGLATGGRQIG--TLIIIPAAGALCS
                                               TVSLWFAKIGSSYLNTWLQKNTTWKKDTICKVLNSIGSIGLGVFLLAATFLDNEHAWMAV
                                                                                                                                                                                -SKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYISSVYHVNIRDNGLLSALP
                                                                                                                                                                                                                             QTEIFGGWPSIFYLSGFIGVLFIFSYIFLGADKPSKQSCISDNELKFITISNQSEDVGKK
                                                                                                                                                                                                                                                                                                                                                                                                                IFSAFNAGLLVMLFTGGMADKFNAKYMILVSVAIASLANFTLPWMAPISVYWAIFSRFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VLPVDSFGGLS--
                                                                                                                                      RTERKVPWKNILKSGAVWASVISLVCHEFPLMTLIMFLPSYLHDVHHYHSTENGILSALP
                                                                                                                                                                                                                                                                                                                                                                    -----PAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGCFTAILI---GGFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108;
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Pred. No. 1.
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Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditi;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae;
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-1- SIMILARITY: TO SODIUM/PHOSPHATE COTRANSPORTER
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APVIVPTVSGF1LSQDPEFGWRNVFF1LFAVNLLGLLFYL1FGEADVQEWAKER: : | | | : | : | :: | |: | | | | |
                                                                                                                                                                                   SYYHVNIRDNGLLSALPFIVAWVIGMVGGYLADFLLTKKF-RLITVRKIATILGSLPSSA
                                                                                                                                                                                                                                                                                                                                                                     LGCFTAILIGGFI-----SETL-GWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNHPKQFAWSSIQQGLIYSGQNFGSLFMVITGWQADRLNGKWTIVAAMAFIIVSNAVLPI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CN----FTT IAQNVI---MNITMVAMVNSTSPQSQLND----
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                                                                                                      LIVSLPYLNS--GYITATALLTLSCGLSTLCQSGIYINVLDIAPRYSSFLMGASRGFSSI
                                                                                                                                                      DVLGLSNTVNGLVSALPMAILFLSKCLSASLASYLTANGYLRKTQSCKIFNFIASLGLGI
                                                                                                                                                                                                                                                                          EKEYIISSLKQQ-VG--SSKQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYIS
                                                                                                                                                                                                                                                                                                                                                                                                                     SAGASFALVFFLRVLTGFGDALLS-PASSSLI-----TRWFPPKERPSALGIVTSGRQ
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                                                                                                                                                                                                                                          EEAY INRKIEEENIGKRNNRKNTPWKAIFTSKQVWVAVAALVCHEFPLVIMLQFLPKFFS
                                                                                                                                                                                                                                                                                                                                 IGTLIILPIGGWLCGSDGSKFLGGWPAIFYLSSVVAAAVLVIWVVFSADKPSKHLCISHN
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9 (TrEMBLrel. 09,
AL 56.0 KD PROTEIN
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BLrel. 09, Last annotation update)
KD PROTEIN T09B9.2 IN CHROMOSOME X.
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N: INTEGRAL MEMBRANE PROTEIN (PO
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Pred. No. 2e-15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Submitted
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PAULEY A., MAGGI L.;
Submitted (MAY-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Rukarvota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-1997) to the ENEMBL; AF003138; AAB54134.1; -
PFAM; PF00083; SUGGAT_L; 1.
SEQUENCE 499 AA; 54949 MW;
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01-NOV-1998
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
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                    PEFGWRNVFFLLFAVNLLGLLFYLIFG
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WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HANKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN K
SMALDON N., SMITH A., SONHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WAATSON R.,
WAATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
                                                                                                                                                                                                                TIVRATPYMKIILNGCVCAICACSFAQSFVLVALVTYLPKYNQIAFKMNLTHNGIWSSLP
                                                                                                                                                                                                                                         AMLRSLP-----IWSICLGCFSHQWLVSTMVVYIPTYISSVYHVNIRDNGLLSALP
                                                                                                                                                                                                                                                                                                                       GWPLVFIVYGLIGAVFLVIWHVRLADKPRESKYITATELTYI--
                                                                                                                                                                                                                                                                                                                                                                      GWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWISTSEKEYIISSLKQQVGSSKQPLPIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPAKSSILGGQFAIWERWGPPQERSRLCSIALSGMLLGCFTAILIGGFISETL-----
VQLSIIVSMAAFSAYVPGYNTSIVTVAPQFTAFISSYAQLYAQIASTLAPIVIGRITSHG
                                                  LTLSCGLSTLCQS----GIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQD
                                                                                                         FFIQMITKLLFAIIADKVKQRKVNATAVTKVSNAIASFASAIFIVIAAY---GPFDSAEL
                                                                                                                                                         FIVAWVIGMVGGYLADFLLTKKFRLITVRKIATILGSLPSSALIVSLPYLNSGYITATAL
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Rhabditidae; Peloderinae;
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-PHOSPHATE TRANSPORTER.
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No. 1.8e-14;
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oderinae; Caenorhabditis.
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
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SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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MEDLINE; 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nemata
Rhabditina; Rhabditoidea;
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 393
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                                                      KDVLMLDVQSNGFYSAIPHISNLIAKLIWGYLMDKMRHKKILSPSATVKLSQFASMMG--
                                                                                                                                                                                               SIALSG-MLLGCFTAILIGGFISETLGWPFVFYIFGGVGCVCCLLWFVVIYDDPVSYPWI
                                                                                                                                                                                                                                                                                   DDGESCTKLEGKVIKDYGGTFIWSVSWQGYIVSAAFLGGFIFSYPAGVLVDRFSARHILS
                                                                                                                                                                                                                                                                                                                                         MCQMTAHIGLSLSCMCNSTAVA---LMNTNNATLVEGTESTILMSILENKTSESQELGGG
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                           PSSALIVSLPYLNSGYITAT --- - ALLTLSC ---- - GLSTLCQSGIYINVLDIAPRYSSFL
                                                                                  SSVYHVNIRDNGLLSALPFIVAWVIGMVGGYLADFLLTKKF----RLITVRKIATILGSL
                                                                                                               HKRELDYLANNIPPKHPSSVVKKTPWRDMLTSKVFWSLMFNSVMGNMMIALIFVYIPVYF
                                                                                                                                        STSEKEYIISSLKQQVGSS-KQPLPIKAMLRSLPIWSICLGCFSHQWLVSTMVVYIPTYI
                                                                                                                                                                      SVFTAGNQLSGMFGNILVAELCASSFGWSSIFYSASLFGISWLVLWHLTVRNSPHNTRWI
                                                                                                                                                                                                                            VAILMLTIASLLMPVLSIYIGEKGAFAGRFVMGISETMLIPSINSMVTKWIPINEKSLAA
 -ISVSCFFLRYMN---
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oidea; Rhabditidae; Peloderinae;
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22.98;
 -CATPFYALVLLSSVSAFFGLSI--
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o_the EMBL/GenBank/DDBJ databases
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annotation update)
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derinae; Caenorhabditis.
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SGFYTSLLSIAPSHIGTL
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Best Local S
Matches 82
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BONFIELD J., BURTON J., CONNELL M., COPEST J., COULS
CORAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER M., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNK
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIAN K., WAYTENSTON R.
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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Q23576;
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DU Z., LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Enkarvota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TremBirel. 01, Created)
01-NOV-1996 (TremBirel. 08, Last sequence update)
01-NOV-1998 (TremBirel. 08, Last annotation update)
01-NOV-1998 (TremBirel. 08, Last nontation update)
SIMILAR TO SODIUM/PHOPHATE TRANSPORTER. NCBI GI: 1086815.
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[2]
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"2.2 Mb of contiguous nucleotide sequence
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EFGWRNVFFLLFAVNLLGLLFYLIFGEADVQEW |: || : |: |: || | : |:|
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                                                                                  LIC--LAMCFVSGYIPGYNTSAVTIAPGQTAAIAAFSRFWGQIASSVAPYHIGAYTKQGT
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82; Conser
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Rhabditoidea; Rhabditidae; Pelo
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24.6%;
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Pred. No. 9.2e
70; Mismatches
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oderinae; Caenorhabditis.
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RESULT CONTROL OF THE Q93599
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MEDLINE; 92168156.

SULSTON J., DU Z., THOMAS K., WILSON R., HILLIER
HALLORAN N., GREEN P., THIERRY-MIEG J., QIU L., D
CRAXTON M., DURBIN R., BERKS M., METZSTEIN M., HA
AINSCOUGH R., WATERSTON R.;
The C. elegans genome sequencing project: a beginature 356:37-41(1992).
                                                                    01-FEB-1997 (TIEMBLIEL.
01-FEB-1997 (TIEMBLIEL.
01-JAN-1999 (TIEMBLIEL.
TZ8F3.4 PROTEIN.
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Q23558;
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Eukaryota; Metazoa; Nematoda;
                                                 T28F3.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1993) to the EMBL; L14429; AAA28211.1; -. SEQUENCE 420 AA; 46281 MY
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STRAIN-BRISTOL N2;
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  Eukaryota; Metazoa;
                      Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                         AHIFSGSIFLLFGSGELQDWAK
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6 (TremBirel. 01,
8 (TremBirel. 08,
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  Nematoda;
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                        Created)
Last sequence update)
Last annotation updat
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Pred. No. 1.2e-12;
2; Mismatches 166;
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Secernentea; Rhabditia; Rhabditida;
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DEAR
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S., COU
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ANDERSON K., BAYNES C., BERKS M.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON I.,
RA GRANDER A., GREEN P., HAMKINS T., HILLIER L., JIER M., JOHNSTON L.
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRILLE P.
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLACHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
A THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K

WATSON A., WEINSTOCK L., WILKINSON-CONTROL
P. 2.2 Mb of Contiquone C. MIKINSON-CONTROL
P. 2.2 Mb of Contiquone C. MIKINSON-CONTROL
P. 2.2 Mb of Contiquone C. MIKINSON-CONTROL
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Best Local S
Matches 81
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Q23063;
Q1-NOV-1996
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Submitted
   NELSON J.,
Submitted (
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                                                                     STRAIN-BRISTOL
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                                                                                  Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPANNAILA-----NWFPSAERSTAISLFTTGNQMAGAGGNPVAASLCASSFGWPSIF
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   WOHLDMANN (JUL-1996)
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PHOSPHATE COTRANSPORTERS
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74; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [3]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
WATERSTON R.;
WATERSTON R.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64609; AAB04605.1; -.
EMBL; U64609; AAB04605.1; -.
SEQUENCE 478 AA; 54373 MW; OBE6E4AO CRC32;
                                                                                                                                                                                                                                                                              425 ITVVITSILYTLFSRATPAEWTMKKR 450
                                 372 AVNLLGLLFYLIFGEADVQEWAKERK 397
                                                                369 ICSRTIQIR----AGQHSHFALNLNMVIAGIAQILIPLGVQAAVPENTRSQWSFVFYFLV 424
                                                                                        312 LCQSGIYINVLDIAPRYSSFLMGASRGFSSIAPVIVPTVSGFLLSQDPEFGWRNVFFLLF 371
                                                                                                                                     309 HVKECYVKFGCGPKLTLVVPLLILESMSAFSLFLTGFLDDRVWSLIFMMIFASLHFFVPV 368
                                                                                                                                                           254 L--AMIVYQQYSPTFIKQVLHFTIRETGYFSAIPQLIAIFIKIGCGRLLDLFM---IFFL 308
                                                                                                                                                                                                                                212 LVSTMVV---YIPTYISSVYHVNIRDNGLLSALPFIVAMVIGMVGGYLADFLLTKKFRLI 268
                                                                                                                                                                                                                                                                                                                                                      138 RWTPESEASFFFSIMLATSQFGPLFTMILGGEMCSSSFFGWEATYYIL-GVGTFISSTAF 196
                                                                                                                                                                                                                                                                                                                                                                            95 RWGPPQERSRLCSIALSGMLLGCFTAILIGGFI--SETLGWPFVFYIFGGVGCVCCLLWF 152
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Search completed: May 25, 2000, 14:51:46 Job time: 2442 sec

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gb_est18:AA675103
gb_est2:AA116763
gb_est2:A1122455
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gb_est3:AA13316149
gb_est2:AA13316149
gb_est2:AA13316149
gb_est2:AA13333978
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9b_est45: AW261723

9b_est29: A1552795

9b_est12: AA276173

9b_est27: A1427938

9b_est34: A1790260

9b_est34: A1790260

9b_est37: A1957130

9b_est10: AA306766

9b_est18: AA706766

9b_est18: AA706766

9b_est18: AA706766

9b_est19: AA688000

9b_est9: AA104847

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Query: US-09-391-958-1
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-Q-/CgP2_1/USPTQ_spool/US09391958/runat_24052000_213329_7148/app_query.fasta.1
-DB-EST -QFMT-fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MIMMATCH=0.100 -LOOPELT=0.000 -LOOPEXT=0.000 -GAPOP=4.50C
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=DIOSum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR_SCORE=pct -ALIGN=15 +MODE=LOCAL
-OUTFMT=pfs -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US09391958
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
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Copyright (c)
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Compugen Ltd.
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gb_est44:AW184318
gb_est21:AA986929
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ACCESSION
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alignment_block:
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 30, 1999 this sequence version replaced gi
Other_ESTs: um91e02.yl
Contact: Marra M/WashU-NCI Mouse EST Project 1999
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 685)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
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                                                                       Quality:
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Fax: 314 286 1810
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h quality sequence stop: 48
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2332154"
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4.051
90.722
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/sex="female"
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                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 641)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Underwood, R., Schurk, R., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Waterston, R., R., Marterston, R., R., Marterston, R., and Wilson, R., Waterston, R., 
                                                                                                                                                                                                                                                                                                   house mouse.
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTGGCTGGCAGATTTTCTACTGAGCAAGAATNTTAGGCTCATAACTGT
ThrLeuSerCysGlyLeuSerThrLeuCysGlnSerGlyIleTyrIleAs
                                                                                                                                                                                                                                                                        CGGCTCTGCCCTATATCCAATCCAGCTATATTACAACAATTATATTTCTG
                                                                                                                                                                                                                                                                                                                                 alSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                            GAGAAAATTCATCACACTTNTAGGAAATGCTCCTCCTGCAGCCCTCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lArgLysIleAlaThrIleLeuGlySerLeuProSerSerAlaLeuIleV
                                                                                                                                       on Mar 16, 1998 this sequence version replaced gi:2961894. Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone this read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissuc_type="whole skin"
/tissuc_type="whole skin"
/dev_stage="11 weeks old"
/dev_stage="11 weeks old"
/lab_host="$OLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
ccoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
ccoRI; Site_2: XhoI; Site
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="MAAGE:522551"
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3.766
87.912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLeuLe 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
On Sep 12, 1996 this sequence version replaced
Contact: Marra M/Mouse EST Project
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 495)
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EST.
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AA276173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                   124
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             /strain="BALB/c"
/db_xref="taxon:10090"
/clone="IMAGE:776148"
                                                                                                                                                                                     /lab_host="DH108"
                                                                                                                                                                                                  /tissue_type="Kidney"
/dev_stage="6 weeks"
                                                                                                                                                                                                                                         /sex="mixed"
                                                                                                                                                                                                                                                            /clone_lib="Barstead MPLRB1"
                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                             Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Louis,
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Mus.
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alignment_block:
US-09-391-958-1
                                                                                                                                                                                    SOURCE
ORGANISM
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KEYWORDS
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LOCUS AI427938
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Percent Similarity:
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          TITLE
                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 452)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                    mm25d12.x1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:522551 3' similar to TR:000476 000476 SODIUM PHOSPHATE TRANSPORTER. ;, mRNA sequence.
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AI427938.1 GI:4273864
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                                                             Schurk, R.,
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JOURNAL
COMMENT
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US-09-391-958-1 x AI427938
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                  158
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                                                                                                                                 206
                                                                                                                                                                                                  156
306
                                                                256
                                                                                                241
                                                                                                                                                               224
                                                                                                                                                                                                                                 208
                                                                                                                                                                                                                                                                                                                                56 ATCCTCTGAACCAACAGTTCAGCTCAGAAGAGCAGCCACTTCCCCATCA 105
                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                 eSerSerLeuLysGlnGlnValGlySerSerLysGlnProLeuProIleL 191
                                                                                                                                                                                                                                                                                                                                                                                                                    AspProValSerTyrProTrpIleSerThrSerGluLysGluTyrIleIl 174
                                                                                                                                                   eSerSerValTyrHisValAsnIleArgAspAsnGlyLeuLeuSerAlaL 241
                                                                                                                                                                                                                                                                                                                                                                                                  GACCCTGTCTCTCACCCATGGATAAGTGGCCCAGAAAGAGAATATATTTT
                                                                                                                                                                                                                   SerHisGlnTrpLeuValSerThrMetValValTyrIleProThrTyrIl 224
AspPheLeuLeuThrLysLysPheArgLeuIleThrValArgLysIleAl 274
                                                                                euProPheIleValAlaTrpValIleGlyMetValGlyGlyTyrLeuAla 257
                                                                                                                                   CAGTTCTGTATTCAAAGTTAACATCAGAGACAATGGGTTCCTGTCTTCTC
                                                                                                                                                                                              ## ACCCATCAGTGGCTTGTTAACACCTTTATAATGTACACTCCAACCTACAT
                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
On Feb 17, 1998 this sequence version replaced gi:2889559.
Contact: Maara M.Washu-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 400.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone was previously sequenced on data is from the 3' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    data is from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouseest@watson.wustl.edu
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3.985
91.946
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/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Stratagene mouse skin (#937313)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:522551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="females"
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SOURCE
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                                                                            alignment_block:
US-09-391-958-1 x AA073942
                                                                                                                                                                                                                                                                                          alignment_scores:
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ORIGIN
                                                                                                                                                                                   Ratio:
Percent Similarity:
Align seg 1/1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 aThrIleLeuGlySerLeuProSerSerAlaLeuIleValSerLeuProT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 yrLeuAsnSerGlyTyrIleThrAlaThrAlaLeuLeuThrLeuSer 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 455)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuqu Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:323357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
washingthm University School of MedicineP
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: -28ml3 revl ET from Amersham High quality sequence stop: 447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                105
                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: heart; Vector: pBluescript SK-; Site_1:
/note="Organ: An in the state of the st
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       AA073942
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/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:536421"
/clone_lib="$tratagene mouse heart (#937316)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                       525.00
3.804
91.391
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           from:
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Gaps:
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ACCESSION
VERSION
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LOCUS AI790260
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 IleValProThrValSerGlyPheLeuLeuSerGlnAspProGluPheGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 rLysLysPheArgLeuIleThrValArgLysIleAlaThrIleLeuGlys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euPheTyrLeuIlePheGlyGluAlaAspValGlnGluTrpAlaLysGlu 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTrpArgAsnValPhePheLeuLeuPheAlaValAsnLeuLeuGlyLeuL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI790260 583 bp mRNA musculus uk57h12.x1 Sugano mouse kidney mkia Mus musculus IMAGE:1973159 3' similar to SW:RPT4_HUMAN 000476 PHOSPHATE TRANSPORT PROTEIN 4; mRNA sequence.
                                                                                                                                                                                                                                                Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R. Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                            Washington University School of Medicine
                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                   On Jun 5, 1998 this sequence version replaced gi:3189727 Other_ESTs: uk57h12.y1
                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                      karyota; Metazoa; Chordata; Craniata; Vertebrata;
theria; Rodentia; Sciurognathi; Muridae; Murinae;
(bases 1 to 583)
                                                                      314 286 1800
314 286 1810
                                                                                                              St. Louis,
                                                                                                              MO
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                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 sileAlaThrileLeuGlySerLeuProSerSerAlaLeuIleValSerL
                                                             aValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyGluAlaAspV 389
                                                                                                                                                                                                                                                                                          uaspilealaproargTyrSerSerPheLeuMetGlyalaSerArgGlyp 339
||||||||||||||||||
| AGACATTGCTCCAAGGTATGCCAGCTTTCTCATGGGAACATCAAGAGGGAT 319
                                                                                                                                                                                                                                                                                                                                                                                    euProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeuLeuThrLeu 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCATCACACTTTTAGGAAATGCTCCTCCTGCAGCCCTCGTTGCGGCTC
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                     AGTTAACCTACTTGGCTTAATCATCTACCTCGTGTTTGGGAAAGCAGATG
                                                                                                                                      SerGlnAspProGluPheGlyTrpArgAsnValPhePheLeuLeuPheAl
                                                                                                                                                                                                                               heSerSerIleAlaProValIleValProThrValSerGlyPheLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCCCTATATCCAATCCAGCTATATTACAACAATTATATTTCTGACAATT
                                                                                                                                                                                                        TGGCACATTCATCGGCTGTGCTGGTACCCATTGTTGCTGGCTTTTTCCTC
                                                                                                              AGCCAGGACTCTGAATTCGGGTGGAGGAATTTCTTTTTTTGTAGTGTTTTGC
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from: ۲

<u>:</u>

452

402

352 362 202

COMMENT

372

269

219

169

355

419

469 289

SOURCE KEYWORDS

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alignment_block:
US-09-391-958-1 x AI790260/rev
                                                                                                                                alignment_scores:
Quality:
                                                                                  Percent Similarity:
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                                                                                                        Ratio:
                                                                                                                                                                                                                                                                  182
                                                                                                                                                                                                                                                                             /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT] double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumlo Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCACCTCGACCACA."
                                                                                                                                                                                                                                                                  ρ
                                                                                516.00
4.000
88.356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:1973159"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex-"female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Sugano mouse kidney mkia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain-"C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism-"Mus musculus
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                                                                             Gaps: 0
Identity: 66.438
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ACCESSION
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KEYWORDS
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AUTHORS
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ORGANISM
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JOURNAL
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542 bp mRNA EST ul75h09.xl Sugano mouse kidney mkia Mus musculus IMACE:2136449 3' similar to SW:NPT4_HUMAN 000476 PHOSPHATE TRANSPORT PROTEIN 4 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 542)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             where ESTs: u175h09.y1
Other ESTs: u175h09.y1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
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On Jun 5, 1998 this sequence version replaced gi:3187888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Possible reversed clone: similarity on wrong strand
                                                     Quality:
Ratio:
                                                                                                                                                   primer: custom primer used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 361.
Location/Qualifiers
                                                                                                                                                           169
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/db_xref="ftaxon:10090"
/clone="TMAGE:2136449"
/clone_lib="sugano mouse kidney mkia"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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                                      511.00
3.961
80.625
                         percent Identity: 60.625
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s cDNA clone
6 SODIUM-DEPENDENT
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US-09-391-958-1 x AI957130/rev
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VERSION
KEYWORDS
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AUTHORS
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LOCUS AA858296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 CACTTTAGGAAATGCTCCTCCTGCAGCCCTCGTTGCGGCTCTGCCCTAT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 hrIleLeuGlySerLeuProSerSerAlaLeuIleValSerLeuProTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                 AA858296 609 bp mRNA EST 09-MAR-1998 obl3b06.sl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1323539 3' similar to TR:000476 000476 SODIUM PHOSPHATE TRANSPORTER. ;, mRNA
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 609)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                             EST.
                                                                                                                                                                                                                                                                                                                                                                               AA858296:1 GI:2946598
                                                                                                                                                                                                                                                                                                                                                                                                 AA858296
                                                                                                                            Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2285607.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
                                                                      Emmail: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                          Tumor Gene Index
CDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center DNA Sequencing by: Washington University Genome Sequencing Can be Clone distribution: NCI-CGAP clone distribution information can be
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ACCESSION
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US-09-391-958-1 x AA858296/rev
                                                                                                                                                                                     seq_documentation_block:
LOCUS AA706766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyPheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePh 368
                                                                                                                                                                                                                                                                                                                                                             CTTGCTGTTTGCCGTTAACCTGTTAGGACTACTCTTCTACCTCATATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                        GGATTTCTTCTTAGTCAGGACCCTGAGTTTGGGTGGAGGAATGTCTTCTT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATCAAGAGGATTTTCGAGCATAGCACCTGTCATTGTACCCACTGTCAGC 460
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                                                                                                                                                                                                                                                                                    zi20d11.s1 Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:431349 3' similar to TR:000476 000476 SODIUM PHOSPHATE TRANSPORTER. ; mRNA sequence.
                                                                           AA706766.1 GI:2716684
EST.
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                                     Homo sapiens
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5.070
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118 c 114 g
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JOURNAL
                                                                                                                                                                                     337
                                                                         171
                                                                                                            354
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121
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REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AA706766 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-391-958-1 x AA706766/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                    320 nValLeuAspIleAlaProArgTyrSerSerPheLeuMetGlyAlaSerA
                                                                                                                                                                                                                       271 TGTCGTAGCATTGCTCACAAGGTATTCCAGTTTTCTCATGGGAGCATCAA
uPheAlaValAsnLeuLeuGlyLeuLeuPheTyrLeuIlePheGlyGluA 387
                                                                                LeuLeuSerGlnAspProGluPheGlyTrpArgAsnValPhePheLeuLe
                                                                                                                                                                             rgGlyPheSerSerIleAlaProValIleValProThrValSerGlyPhe
                                                                                                                                           GATGATTTTCGAGCATAGCACCTGTCATTGTACCCACTGTCAGCGGATTT
                                                           CTTCTTAGTCAGGACCCTGAGTTTGGGTGGAGGAATGTCTTCTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l (bases 1 to 321)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Hillier, L., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project
Unpublished (1997)
On May 5, 1995 this sequence version replaced gi:798085.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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4.903
94.898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="GDB:1331118"
/db_xref="taxon:9606"
/clone="IMAGE:431349"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
Percent Identity:
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0
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                                                                                                                                           172
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est24:AI244777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                    alignment_block:
                                                                                                              US-09-391-958-1 x AI244777/rev
                                                                        Align seg 1/1 to reverse of: AI244777
                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                 312 LeuCysGlnSerGlyIleTyrIleAsnValLeuAspIleAlaProArgTy 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTGTCAGTCAGGGATTTATATCAATGTCTTAGATATTGGTCCAAGGTA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1244777 297 bp mRNA EST 28-JAN-119 qj92f01.xl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1866 similar to SW:NPT4_HUMAN 000476 SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 4 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 297)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jan 19, 1998 this sequence version replaced gi:2045043. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: -400P from Gibco
High quality sequence stop: 156.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length: 707
                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                   Ratio
                                                                                                                                                                                                                                                                                                                     94
                                                                                                                                                                                                                                                                                                                             /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with mote="Torgan: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I primer (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon.9606"
/clone="IMAGE:1866937"
/clone_lib="NCI_CGAP_Kid3"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                              452.00
5.079
98.889
                                                                                                                                                                                                                                                                                                                     68 c
                                                                                                                                                                              Length: 90
Gaps: 0
Percent Identity: 97.778
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                                                                                                                                                                                                                                                                                                                           1 others
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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ORGANISM
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362 GlyTrpArgAsnValPhePheLeuLeuPheAlaValAsnLeuLeuGlyLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allleValproThrValSerGlyPheLeuLeuSerGlnAspProGluPhe 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTCTTCTACCTCATATTTGGAGAAGCAGATGTCCAAGAATGGGCTAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA985952 632 bp mRNA EST 28-MAY-1998
AA985952 632 bp mRNA mus musculus cDNA clone
uc72909.xl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1431232 3' similar to SW:NT74_HUMAN 000476 SODIUM-DEPENDENT
PHOSPHARE TRANSPORT PROTEIN 4 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 632)

1 (bases 1 to 632)

Narra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucabb, T., Lacy, M., Le, M., Martin, J., Morris, M., Geisel, S., Kucabb, T., Lacy, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, R., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Wasterston R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
On Jan 14, 1998 this sequence version replaced gi:17970:
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA985952.1 GI:3167341
                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity on 
Seq primer: primer name ambiguous 
High quality sequence stop: 471. 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mmail: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
/note-"Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACCATGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer and primed with an oligo(dT) primer and cloned into distinct DraIII sites of the pME18S-FL3 and cloned into distinct DraIII sites of the pME18S-FL3
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                        /dev_stage="adult"
                                                                                                                                                                                                                                           /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:1431232"
                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL"
                                                                                                                                                                                  /lab_host="DH10B"
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ACCESSION
VERSION
KEYWORDS
SOURCE
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US-09-391-958-1 x AA985952/rev
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                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                        400
                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                            384 PheGlyGluAlaAspValGlnGluTrpAlaLysGluArgLysLeuThrAr 400
                                                                                                                                                                                                                                                                                                                                                                                                                     367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 AlaLeuIleValSerLeuProTyrLeuAsnSerGlyTyrIleThrAlaTh 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 gLysIleAlaThrIle.LeuGlySerLeuProSer......ser 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625 TGGTTGGCAGATTTTCTACTGAGCAAGAT.TTTAGGCTCATACTTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 TyrLeuAlaAspPheLeuLeuThrLysLysPheArgLeuIleThrValAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyAlaSerArgGlyPheSerSerIleAlaProValIleValProThrVa
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                                                                                                                                                                                                                                    TTTG 173
                                                                                                                                                                                                                                                                        gLeu 401
                                                                                                                                                                                                                                                                                                           TTTGGGAAAGCAGATGTTCAAGAATGGGCTAGAGAGGAAGCTCACTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCTGGCTTTTTCCTCAGCCAGGACTCTGAATTCGGGTGGAGGAATTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lSerGlyPheLeuLeuSerGlnAspProGluPheGlyTrpArgAsnValP 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAACATCAAGAGGATTGGCACATTCATCGGCTGTGCTGGTACCCATTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAATTCATCACACTTTAGAAATGCTCTCCGCAGCCTGTTGNNCCCCGGG
                                                                                                                                                                                                 gb_est37:AW011903
                                                                                                    AW011903 540 bp mRNA EST 10-SEP-1999 uml1b06.xl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2182739 3', similar to SW:NP74_HUMAN 000476 SODIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                            PHOSPHATE TRANSPORT PROTEIN 4 ;, mRNA sequence AW011903
     Mus musculus
                                                         AW011903.1 GI:5860681
                      louse mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to reverse of: AA985952 from: 1
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                                                  490 TACAACAATTATATTTCTGACAATTTCCTGTGGACTGTGCCCTCTATCTC
                                                                                                                                                                                                                             281 ProSerSerAlaLeuIleValSerLeuProTyrLeuAsnSerGlyTyrIl
                                                                                                                                                          297 eThrAlaThrAlaLeuLeuThrLeuSerCysGlyLeuSerThrLeuCysG
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Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1004407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1133842.
Contact: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 540)
Marra, M., Hillier, L., Kucaba, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                 constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACCATGTGTG); Site_2: DraIII (CACCATGTGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACCGTGTG, 3' site CACCATGTG). XhoI show be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2182739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Sugano mouse kidney mkia"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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seq_documentation_block:
LOCUS AA104847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrLeuIlePheGlyGluAlaAspValGlnGluTrpAlaLysGluArgLy 397
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AA104847
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1996)
On Apr 14, 1993 this sequence version replaced On Apr 14, 1993 this sequence version replaced Contact: Marra M/Mouse EST Project Washu-HMI Mouse EST Project Washington University School of MedicineP Washington University Published Washington University School of MedicineP Washington University Published Washington University School of MedicineP Washington University Published Washington University Publishe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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h quality sequence stop: 421
                 109
    3']; double-stranded cDNA was ligated to Eco RI adaptors [CATGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
134 c 92 g 144 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="BALB/C"
                                                                                                                                                                                                            /clone_lib="Barstead MPLRB1"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:571746"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
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further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mm25d12.rl Stratagene mouse skin (#937313) Mus musculus cDNA clone rMaGE:522551 5' similar to TR:G165690 G165690 RENAL CORTICAL NA/P-I-COTRANSPORTER. ;, mRNA sequence.
                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Align seg 1/1 to: AA104847
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seq_name: gb_est9:AA068000
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                                                                                                                                                                                                                                                                                                                                                                                                  177 euLysGlnGlnValGlySerSerLysGlnProLeuProIleLysAlaMet 193
                                                                                                                                                                                                                                                                                                                                                    194 LeuArgSerLeuProIleTrpSerIleCysLeuGlyCysPheSerHisGl 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 lSerTyrProTrpIleSerThrSerGluLysGluTyrIleIleSerSerL 177
                                                                                                                                                                                                                                                                              201 ATGGTCGAACAGTCTCCTGGTTACATACACGCCGACATTTATCAGCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                              260 uLeuThrLysLys...PheArgLeuIleThrValArgLysIleAlaThrI 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGGTGTGTTCTGAGTCTTTCCTGGTTCTTTCTATTCTTTGATGACCCCAA
                                                                           276 leLeuGlySerLeuProSerSerAlaLeuIleValSerLeuProTyrLeu
                                                                                                                                                                                                                                                                                                                                                                             nTrpLeuValSerThrMetValValTyrIleProThrTyrIleSerSerV
                                                                                                                                                                                                                                                                                                                               CTGCTTGCCTACATCTGTGGTATCCTAGCAGGTCAGATGTCAGACTTCTT
                                                                                                                                                                                                     IleValAlaTrpValIleGlyMetValGlyGlyTyrLeuAlaAspPheLe
                              AGCTACAACTTC 462
                                                   AsnSerGlyTyr 296
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alignment_block:
US-09-391-958-1 x AA068000/rev
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ValGlnGluTrpAlaLysGluArgLysLeuThrArgLeu 401
                                                                                                                                                                                                                                                                                                               uSerGlnAspProGluPheGlyTrpArgAsnValPhePheLeuLeuPheA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCCTGTGGACTGTGCCCTCTATCTCAGGCAGGAATCTATATTAATGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGCCCTATATCCAATCCAGCTATATTACAACAATTATATCTCTGACAAT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuProTyrLeuAsnSerGlyTyrIleThrAlaThrAlaLeuLeuThrLe
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Possible reversed clone: similarity on wrong strand
Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 314.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1996)
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/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
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/dev_stage="11 weeks old"
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/sex="females"
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/strain="C57BL/6"
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/clone="IMAGE:522551"
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alignment_block:
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                                                   112 yMetLeuGeuGlyCysPheThrAlaIleLeuIleGlyGlyPheIleSerG 129
                                                                                                                                                                    96 TrpGlyProProGlnGluArgSerArgLeuCysSerIleAlaLeuSerGl
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                                                                                                             TGGGCTCCGCACTTGGAACGGAGCAAGCTCACCAGCATTGCGTGTTCA..
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AA675103
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1 (bases 1 to 462)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thoisista B., Wolfe, M., Steptoe, M., Tan, F., Underwood, K., Moore, B., Tan, F., Underwood, K., Moore, B., Tan, F., Underwood, K., Moore, B.,
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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On Sep 12, 1996 this sequence version replaced gi:1405024
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:599418
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h quality sequence stop: 433.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oliqo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                             416.00
3.382
68.715
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/tissue_type="diaphragm"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
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